

GenCore version 4.5
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0M protein protein search, using SW model

Run on: August 12, 2002, 14:11:59 : Search time 24.79 seconds
(without alignments)
304,458 Million cell updates/sec

Hit: US-09-825-882-8
Footest score: 1597
Sequence: 1 MITEPLIPFSSLVVTEVIG.....FLNFWQMRWVRKSPKISSP 309

Sorting table:
RUSUM02
Gapex 10.0 : Gapex1 0.5

Sorted: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: Issued_Patents_AA:*
2: US-09-825-882-8
3: US-09-825-882-8
4: US-09-825-882-8
5: US-09-825-882-8
6: US-09-825-882-8

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length DB	ID	Description
1	140.5	8.2	380 1	US-08-153-848-40 Sequence 40, Appl
2	140.5	8.2	380 3	US-09-299-843A-40 Sequence 40, Appl
3	140.5	8.2	380 4	US-09-088-4378-40 Sequence 40, Appl
4	140.5	8.2	380 5	PCT-US93-11153-40 Sequence 40, Appl
5	125	7.8	454 1	US-08-570-157-7 Sequence 7, Appl
6	124	7.7	454 4	US-08-875-573-20 Sequence 29, Appl
7	124	7.7	454 4	US-09-332-878-2 Sequence 2, Appl
8	124	7.7	454 4	US-09-045-583-55 Sequence 55, Appl
9	117.5	7.4	425 1	US-08-118-270-51 Sequence 51, Appl
10	117.5	7.4	425 5	PCT-US93-08528-51 Sequence 51, Appl
11	115	7.2	476 4	US-08-387-707-17 Sequence 17, Appl
12	114	7.1	488 1	US-08-446-822-8 Sequence 8, Appl
13	114	7.1	488 5	PCT-US93-12586-8 Sequence 8, Appl
14	111.5	7.0	464 1	US-08-148-209A-2 Sequence 2, Appl
15	110.5	6.9	464 1	US-08-148-209A-3 Sequence 3, Appl
16	108.5	6.8	487 1	US-07-996-772A-2 Sequence 2, Appl
17	108.5	6.8	487 5	PCT-US93-12586-2 Sequence 2, Appl
18	108.5	6.8	487 5	PCT-US93-12586-2 Sequence 2, Appl
19	106.5	6.7	437 1	US-08-153-848-46 Sequence 46, Appl
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21	106.5	6.7	437 4	US-09-088-4378-46 Sequence 46, Appl
22	106.5	6.7	437 5	PCT-US93-11153-46 Sequence 46, Appl
23	106.5	6.7	452 1	US-08-202-056-3 Sequence 4, Appl
24	106.5	6.7	452 1	US-08-076-093A-4 Sequence 4, Appl
25	106.5	6.7	452 1	US-08-701-265-4 Sequence 4, Appl
26	106.5	6.7	452 2	US-08-284-586-4 Sequence 4, Appl
27	106.5	6.7	452 2	US-08-805-478-4 Sequence 4, Appl

ALIGNMENTS

28	106.5	6.7	452 2	US-08-802-627A-4 Sequence 4, Appl
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39	106	6.6	380 4	US-09-113-426-5 Sequence 5, Appl
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42	105.5	6.6	361 3	US-09-178-647-2 Sequence 2, Appl
43	105	6.6	380 3	US-08-676-351-5 Sequence 5, Appl
44	105	6.6	380 4	US-08-765-713-2 Sequence 2, Appl
45	105	6.6	404 4	US-09-045-583-2 Sequence 2, Appl

RESULTS

US-08-153-848-40
Sequence 40, Application US/08153848

Patent No. 5759804

GENERAL INFORMATION:

APPLICANT: Godiska, Ronald

APPLICANT: Gray, Patrick W.

ATTORNEY: S.W. Carr, Venable

INVENTOR: S.W. Carr, Venable

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:

ADDRESS: Barnhill, Steele, Gerstle, Murray &

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ADDRESS: Barnhill, Steele, Gerstle, Murray &

Query Match: 8.2%, Score 140.5, DB 1: Length 300;
Post Local Similarity: 19.0%, Prod. No. 2, 1e-05;
Matches: 66, Conservative: 77, Mismatches: 127, Indels: 77, Gaps: 10


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07 150 PLEPTESSIVVTVTINPFAVPIAVNSIFKPKPT SPADQITTAIVS----- 62
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RESULT 8
US-09-045-584-55
Sequence 55, Application US-09-045-584
Patent No. 6287805
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESS: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patcom in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-09-045-584
FILING DATE: 20 MAR-96
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 46,297
REFERENCE/AGENT NUMBER: PNT-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
US-09-045-584-55

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Query Match 7.78; Score 124; DB 4; Length 360;
 Best Local Similarity 18.58; Prod. No. 0.00012;
 Matches 43; Conservative 62; Mismatches 105; Indels 119; Gaps 11.

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RESULT 9
US-08-118-270-51
Sequence 51, Application US-08-118-270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
TITLE OF INVENTION: PEPTIDES OF G-COUPLED PROTEIN
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESS: BROWDY AND NEWMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patcom in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-08-118-270
FILING DATE: 09-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,044
REFERENCE/AGENT NUMBER: MURPHY 2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5192
TELEFAX: 202-747-4528
TELEX: 248634
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-51

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Query Match 7.44; Score 117.5; DB 1; Length 325;
 Best Local Similarity 24.18; Prod. No. 0.00007;

RECEIVED TO
 OCT 05 1964 08:28 A.M.
 INVENTOR: S. L. APPELTON 1001 WYCHWOOD AVE
 GENERAL INFORMATION:
 APPLICANT: New York University
 TITLE OF INVENTION: POLYPEPTIDES OF C-CADHERIN PROTEIN
 FIELD OF INVENTION: RECEPTORS, AND COMBINATIONS AND METHODS THEREOF
 NUMBER OF SEQUENCES: 148
 CORRESPONDENT'S ADDRESS:
 ADDRESS: BROOKLYN AND NEWMARK
 STREET: 410 SEVENTH STREET, N.W., SUITE 400
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 FILING DATE: 1964
 NUMBER OF CLAIMS: 6
 MEDIUM TYPE: FLUORESCENT DISK
 NUMBER OF DRAWINGS: 10
 TREATMENT SYSTEM: 100 DAYS/MS 10S
 SOFTWARE: Program to be loaded #1.10, Version #1.15
 COMMENTS: 1. Filed in U.S. Pat. #2,970,000
 2. Filed in U.S. Pat. #2,970,000
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 150. Filed in U.S. Pat. #2,970,000

RESULT 11
 US-08-487-707-17
 Sequence 17, Application 08/08487707
 Patent No. 6,265,664
 GENERAL INFORMATION:
 APPLICANT: EVANS, CHRISTOPHER J.
 APPLICANT: KEITH, IRVINE E.
 TITLE OF INVENTION: OPLOID RECEPTOR GENES
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOKESLER
 STREET: 2000 Pennsylvania Avenue, N.W., Suite 5500
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20006-1888
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 EXEMPTION: 108 IN COMPLIANCE
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patched to Release #1.0, Version #1.40
 CONTACT ATTORNEY/AGENT DATA:
 APPLICATION NUMBER: 08/087077
 FILING DATE: 10 SEP 1996
 CLASSIFICATION: 5.06
 ATTORNEY/AGENT INFORMATION:
 NAME: MORRISON, KATE H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/WORK KEY NUMBER: 22003-20520, 20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-0764
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 476 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-487-707-17

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Query Match      7.26; Score 115; Dbl 4; Length 47;
Best Local Similarity 18.6%; Pred. No. 0.0008;
Matches 60; Conservative 85; Mismatches 15; Totals 44; Gaps 14;
5. LPIIPSTVYVFLVFNAMATLALVNSLFWGRKG ----- KSPADQLITALVNSV G

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GY	5	LEPESVWVVFVYVGNFAMFAL	-----VNSFEMKRGKISFAMQIALAV	54	
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GY	54	SKVELLVLLVLLV	YGVVNVVNSVVFRTAVVIMAV	INDFNNMLATLSTFVL	LKI
Db	99	-----LMAVYVSFTMLDLP	-----VMKVSSTLIMMA	-----SFTFOMSV	IQD
GY	111	ANLVNFTLVHFAVFA	VVNVVGVVGVVFA	GVVVFVGVVGVV	GVVVFVGVV
Db	141	DRGVSVFYVFLNSDRIWLVAVVYVVLVWVMAV	LVNSDRIYV	ISVRIITLVAVAV	LVNSDRIYV

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CY 165 FFFKSAVVS-SMTVMVWAM-VFTTTLTMTTNS-CHLEFPLHFR- 200PST 021
DB 196 -MAFFPERVAQMSA-TAMSNTOSETEPFIATQYHQLZHHUK-INSYGNPILBNQVH 255
QY 222 EVHFKALVTSSTLLEVAIV-LSHLSWWSLQSLNKEVEN-----TKARISYH 272
DB 256 KM- AAAYVLAH-LTQWLFHVLLFLDALIMWGLINSCEVAVIOLALPFAILLGFTNS 311
QY 273 SHHPTLLWNNKLNQTHLSVFWQMRWVWGEN 305
DB 312 QVNEFLVTFVGNPQKLRSVFVVTIMLQKR 344

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Search completed: August 12, 2002, 13:50:04
Job Time: 2285 Sec


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1 SOFTWARE: WordPerfect for Windows, Version 7.0
2 CURRENT APPLICATION DATA:
3 APPLICATION NUMBER: US/06/0005/061
4 FILING DATE:
5 CLASSIFICATION:
6 PRIOR APPLICATION DATA:
7 APPLICATION NUMBER: 09/717,221
8 FILING DATE: No. 6,912,222 December 12, 1996
9 ATTORNEY/AGENT INFORMATION:
10 NAME: Verser, Carol Talkington
11 REGISTRATION NUMBER: 47,459
12 REFERENCE/EXCERPT NUMBER: PC-1
13 TELECOMMUNICATION INFORMATION:
14 TELEPHONE: 970/494-7272
15 TELEFAX: 970/484-9505
16 INFORMATION FOR SEQ ID NO: 15:
17 SEQUENCE CHARACTERISTICS:
18 LENGTH: 1982 nucleotides
19 TYPE: nucleic acid
20 STRANDEDNESS: single
21 TOPOLOGY: linear
22 MOLECULE TYPE: cDNA
23 US-09-065-051-15

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Query Match 1.00, Score 18, Ht 4, Length 1982
Best Local Similarity 100.0% Prod. No. 147
Matches 18, Conserved 0, Mismatch 0, Gaps 0,

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CY 54 TATTGAATTTTCTAA 71
11111111111111111111
DB 260 TATTGAATTTTCTAA 277

```

```

RESULT 5
US-08-747-221B-57/c
1 Sequence 57, Application US/97/7221B
2 Patent No. 6063610
3 GENERAL INFORMATION:
4 APPLICANT: Silver, Gary W.
5 APPLICANT: Wisniewski, Nancy
6 TITLE OF INVENTION: NO. 60661061 Carboxyl-structure No. 10 Acid
7 NUMBER OF SEQUENCES: 66
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Carol Talkington Verser, Ph.D.
10 STREET: 1825 Sharp Point Drive
11 CITY: Fort Collins
12 STATE: Colorado
13 COUNTRY: USA
14 ZIP: 80525
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: floppy disk
17 OPERATING SYSTEM: Windows 95
18 SOFTWARE: WordPerfect for Windows, Version 7.0
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/08/747,221B
21 FILING DATE: No. 6063610 December 12, 1996
22 CLASSIFICATION: 435
23 ATTORNEY/AGENT INFORMATION:
24 NAME: Verser, Carol Talkington
25 REGISTRATION NUMBER: 47,459
26 REFERENCE/EXCERPT NUMBER: PC-1
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: 970/494-7272
29 TELEFAX: 970/484-9505
30 INFORMATION FOR SEQ ID NO: 57:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 2144 nucleotides
33 TYPE: nucleic acid
34 STRANDEDNESS: single
35

```

```

1 TOPOLOGY: linear
2 MOLECULE TYPE: cDNA
3 FEATURE:
4 NAME/KEY: CDS
5 LOCATION: 30..1682
6 FEATURE:
7 NAME/KEY: 5' UTR
8 LOCATION: 462
9 US-08-747-221B-57

```

```

Query Match 1.00, Score 18, Ht 4, Length 2144
Best Local Similarity 100.0% Prod. No. 147
Matches 18, Conserved 0, Mismatch 0, Gaps 0,

```

```

CY 54 TATTGAATTTTCTAA 71
11111111111111111111
DB 1885 TATTGAATTTTCTAA 1868

```

```

RESULT 6
US-08-747-221B-59
1 Sequence 59, Application US/98/747221B
2 Patent No. 6063610
3 GENERAL INFORMATION:
4 APPLICANT: Silver, Gary W.
5 APPLICANT: Wisniewski, Nancy
6 TITLE OF INVENTION: NO. 60661061 Carboxyl-structure No. 10 Acid
7 NUMBER OF SEQUENCES: 66
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Carol Talkington Verser, Ph.D.
10 STREET: 1825 Sharp Point Drive
11 CITY: Fort Collins
12 STATE: Colorado
13 COUNTRY: USA
14 ZIP: 80525
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: floppy disk
17 OPERATING SYSTEM: Windows 95
18 SOFTWARE: WordPerfect for Windows, Version 7.0
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/98/747,221B
21 FILING DATE: No. 60661061 December 12, 1996
22 CLASSIFICATION: 435
23 ATTORNEY/AGENT INFORMATION:
24 NAME: Verser, Carol Talkington
25 REGISTRATION NUMBER: 47,459
26 REFERENCE/EXCERPT NUMBER: PC-1
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: 970/494-7272
29 TELEFAX: 970/484-9505
30 INFORMATION FOR SEQ ID NO: 59:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 2144 nucleotides
33 TYPE: nucleic acid
34 STRANDEDNESS: single
35 TOPOLOGY: linear
36 MOLECULE TYPE: cDNA
37 US-08-747-221B-59

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Query Match 1.00, Score 18, Ht 4, Length 2144
Best Local Similarity 100.0% Prod. No. 147
Matches 18, Conserved 0, Mismatch 0, Gaps 0,

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CY 54 TATTGAATTTTCTAA 71
11111111111111111111
DB 260 TATTGAATTTTCTAA 277

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1 09-09-1014-19
2 Sequence 6, Application US/09041014
3 GENERAL INFORMATION:
4 APPLICANT: The Trustees of the City of New York
5 APPLICANT: City
6 TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
7 TITLE OF INVENTION: VIRUS SEQUENCES AND USES THEREOF
8 NUMBER OF SEQUENCES: 45
9 CORRESPONDENCE ADDRESS:
10 ADDRESS: Cooper & Dunham LLP
11 STREET: 1185 Avenue of the Americas
12 CITY: New York
13 STATE: New York
14 COUNTRY: U.S.A.
15 ZIP: 10040
16 COMPUTER RELEASABLE FORM:
17 MEDIUM TYPE: floppy disk
18 COMPUTER: IBM pc compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: Patent in Release #1.25
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: PCT/US95/10104
23 FILING DATE:
24 CLASSIFICATION:
25 ATTORNEY/AGENT INFORMATION:
26 NAME: White Esq., John P.
27 REGISTRATION NUMBER: 28,678
28 REFERENCE TO PCT NUMBER: 45185-A
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: 212-278-0400
31 TELEFAX: 212-278-0400
32 INFORMATION FOR SEQ ID NO: 18:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 1410 base pairs
35 TYPE: nucleic acid
36 STRANDNESS: single
37 TOPOLOGY: linear
38 MOLECULE TYPE: DNA (genomic)
39 HYPOTHEICAL: N
40 ANTI-SENSE: N
41 US-08-343-1014-6
42
43 Query Match: L006: Score 172, 100%, Length 12152
44 Post Local Similarity: 100.00% Prod. No. 412
45 Matches: 172 Conserved pos. 02 Mismatches 02 Indels 02 Gaps 02
46
47 4 database entries
48 DB 623 GATACATTTTCAVVA 751
49
50 RESULT 14
51 US-09-041014-19
52 Sequence 6, Application US/09041014
53 Patient No. 609350
54 GENERAL INFORMATION:
55 APPLICANT: Chaney, Yvonne
56 APPLICANT: Moore, Patrick S.
57 TITLE OF INVENTION: Unique Associated Kaposi's Sarcoma
58 TITLE OF INVENTION: Virus Sequences And Uses Thereof
59 NUMBER OF SEQUENCES: 22
60 CORRESPONDENCE ADDRESS:
61 ADDRESS: Cooper & Dunham
62 STREET: 1185 Avenue of the Americas
63 CITY: New York
64 STATE: New York
65 COUNTRY: U.S.A.
66 ZIP: 10040
67
68 COMPUTER RELEASABLE FORM:
69 MEDIUM TYPE: floppy disk
70 COMPUTER: IBM pc compatible
71 OPERATING SYSTEM: PC-DOS/MS-DOS
72 SOFTWARE: Patent in Release #1.24
73 CURRENT APPLICATION DATA:
74 APPLICATION NUMBER: US/09/1014-008
75 FILING DATE:
76 CLASSIFICATION:
77 PRIOR APPLICATION DATA:
78 APPLICATION NUMBER: 09/041014
79 FILING DATE:
80 ATTORNEY/AGENT INFORMATION:
81 NAME: White Esq., John P.
82 REGISTRATION NUMBER: 28,678
83 REFERENCE TO PCT NUMBER: 45185-A
84 TELECOMMUNICATION INFORMATION:
85 TELEPHONE: 212-278-0400
86 TELEFAX: 212-278-0400

```

```

1 COMPUTER RELEASABLE FORM:
2 MEDIUM TYPE: floppy disk
3 COMPUTER: IBM pc compatible
4 OPERATING SYSTEM: PC-DOS/MS-DOS
5 SOFTWARE: Patent in Release #1.24
6 CURRENT APPLICATION DATA:
7 APPLICATION NUMBER: US/09/1014-01014
8 FILING DATE:
9 CLASSIFICATION: 514
10 ATTORNEY/AGENT INFORMATION:
11 NAME: White Esq., John P.
12 REGISTRATION NUMBER: 28,678
13 REFERENCE TO PCT NUMBER: 45185-A
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE: 212-278-0400
16 TELEFAX: 212-278-0400
17 INFORMATION FOR SEQ ID NO: 6:
18 SEQUENCE CHARACTERISTICS:
19 LENGTH: 1410 base pairs
20 TYPE: nucleic acid
21 STRANDNESS: single
22 TOPOLOGY: linear
23 MOLECULE TYPE: DNA (genomic)
24 HYPOTHEICAL: N
25 ANTI-SENSE: N
26 US-08-343-1014-6
27
28 Query Match: L006: Score 172, 100%, Length 14102
29 Post Local Similarity: 100.00% Prod. No. 412
30 Matches: 172 Conserved pos. 02 Mismatches 02 Indels 02 Gaps 02
31
32 4 database entries
33 DB 623 GATACATTTTCAVVA 609
34
35 RESULT 15
36 US-09-183-608-6
37 Sequence 6, Application US/09183608
38 Patient No. 609350
39 GENERAL INFORMATION:
40 APPLICANT: Chaney, Yvonne
41 APPLICANT: Moore, Patrick S.
42 TITLE OF INVENTION: Unique Associated Kaposi's Sarcoma
43 TITLE OF INVENTION: Virus Sequences And Uses Thereof
44 NUMBER OF SEQUENCES: 22
45 CORRESPONDENCE ADDRESS:
46 ADDRESS: Cooper & Dunham
47 STREET: 1185 Avenue of the Americas
48 CITY: New York
49 STATE: New York
50 COUNTRY: U.S.A.
51 ZIP: 10040
52
53 COMPUTER RELEASABLE FORM:
54 MEDIUM TYPE: floppy disk
55 COMPUTER: IBM pc compatible
56 OPERATING SYSTEM: PC-DOS/MS-DOS
57 SOFTWARE: Patent in Release #1.24
58 CURRENT APPLICATION DATA:
59 APPLICATION NUMBER: US/09/183-608
60 FILING DATE:
61 CLASSIFICATION:
62 PRIOR APPLICATION DATA:
63 APPLICATION NUMBER: 09/041014
64 FILING DATE:
65 ATTORNEY/AGENT INFORMATION:
66 NAME: White Esq., John P.
67 REGISTRATION NUMBER: 28,678
68 REFERENCE TO PCT NUMBER: 45185-A
69 TELECOMMUNICATION INFORMATION:
70 TELEPHONE: 212-278-0400
71 TELEFAX: 212-278-0400

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```

: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 1410 base pairs
:   TYPE: nucleic acid
:   STRANDEDNESS: single
:   TOPOLOGY: linear
:   MOLECULE TYPE: DNA (genomic)
:   HYPOTHETICAL: N
:   ANTI-SENSE: N
:   ORIGIN: 688-688

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Query Match      1.00; Score 17; DB 3; Length 1410;
Post local Similarity 100.00; Prod. No. 41;
Matches 17; Conservation 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 aataattttctatgca 19
11111111111111111111
ID 623 GATAAATTTTCTAACA 639

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Search completed: August 12, 2002, 18:13:07
Job time: 3949 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleotide - nucleotide search, using SW model

Run on: August 12, 2002, 11:34:43 : Search time 49.18 Seconds

(Without alignments)
4644.961 Million cell updates/sec

Title: US-09-825-882-7
Report score: 1.0
Sequence: 1.0
Gapopen: 10.0, Gapext: 1.0

Scoring table:
Gapopen: 10.0, Gapext: 1.0

Search: 48343 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767086

Minimum hit seq length: 0
Maximum hit seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database:

Issued_Patents_NA:
1. US-09-012-030-1 for "A COMPOSITION"
2. US-09-012-030-2 for "A COMPOSITION"
3. US-09-012-030-3 for "A COMPOSITION"
4. US-09-012-030-4 for "A COMPOSITION"
5. US-09-012-030-5 for "A COMPOSITION"
6. US-09-012-030-6 for "A COMPOSITION"

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	40.4	4.3	5622	4	US-09-012-030-1	Sequence 3, Appl
2	40.4	4.3	5622	4	US-09-012-030-2	Sequence 3, Appl
3	36	3.9	7218	1	US-08-248-466B-1	Sequence 14, Appl
4	35.8	3.8	1512	1	US-08-248-466B-2	Sequence 14, Appl
5	35.8	3.8	1512	1	US-08-248-466B-3	Sequence 14, Appl
6	34.8	3.7	3288	1	US-08-208-008C-1	Sequence 11, Appl
7	34	3.7	2989	4	US-09-012-030-6	Sequence 9, Appl
8	34	3.7	2989	4	US-09-012-030-7	Sequence 9, Appl
9	34	3.7	2989	4	US-09-012-030-8	Sequence 9, Appl
10	34	3.6	2629	2	US-09-012-030-1	Sequence 1, Appl
11	34.4	3.5	2629	2	US-08-590-454-1	Sequence 1, Appl
12	33	3.5	14602	1	US-08-597-236-1	Sequence 1, Appl
13	33	3.5	14602	1	US-08-597-236-2	Sequence 1, Appl
14	32.4	3.5	2974	3	US-08-413-522A-7	Sequence 7, Appl
15	32.4	3.5	2974	3	US-09-115-166-7	Sequence 7, Appl
16	32.4	3.5	2974	4	US-08-942-046-7	Sequence 7, Appl
17	32.4	3.5	2974	4	US-08-942-046-8	Sequence 7, Appl
18	32	3.4	3088	1	US-08-947-610-3	Sequence 2, Appl
19	31.6	3.4	276	1	US-07-800-470-1	Sequence 1, Appl
20	31.6	3.4	276	1	US-08-057-169-1	Sequence 1, Appl
21	31.6	3.4	448	1	US-09-027-499-4	Sequence 12, Appl
22	31.6	3.4	468	4	US-09-299-268-47	Sequence 47, Appl
23	31.6	3.4	895	3	US-08-924-747-7	Sequence 7, Appl
24	31.6	3.4	895	3	US-09-247-474B-7	Sequence 7, Appl
25	31.6	3.4	895	4	US-09-296-715-7	Sequence 7, Appl
26	31.6	3.4	4156	1	US-08-465-687A-1	Sequence 1, Appl
27	31.6	3.4	4156	1	US-09-030-970-1	Sequence 1, Appl

28	31.6	3.4	4156	5	PCT-US94-11843-1	Sequence 1, Appl
29	31.6	3.4	14176	1	US-08-407-499-1	Sequence 1, Appl
30	31.6	3.4	14176	1	US-08-407-499-14	Sequence 14, Appl
31	31.6	3.4	14176	4	US-09-299-268-1	Sequence 1, Appl
32	31.6	3.4	14176	4	US-09-299-268-14	Sequence 14, Appl
33	31.4	3.4	840	1	US-08-688-609-1	Sequence 1, Appl
34	31.4	3.4	840	3	US-09-002-852-1	Sequence 1, Appl
35	31.4	3.4	1875	1	US-08-286-425A-1	Sequence 1, Appl
36	31.4	3.4	3234	1	US-08-286-425A-2	Sequence 1, Appl
37	30.8	3.3	458	1	US-09-141-000-4	Sequence 4, Appl
38	30.8	3.3	2454	1	US-08-459-696-3	Sequence 3, Appl
39	30.8	3.3	37948	4	US-09-251-645-11	Sequence 11, Appl
40	30.6	3.3	2965	2	US-08-460-570-1	Sequence 1, Appl
41	30.6	3.3	2965	2	US-08-460-570-2	Sequence 2, Appl
42	30.6	3.3	2965	3	US-08-286-870A-1	Sequence 1, Appl
43	30.6	3.3	2965	3	US-08-286-870A-2	Sequence 2, Appl
44	30.4	3.3	791	2	US-07-645-196A-4	Sequence 4, Appl
45	30.4	3.3	1568	4	US-09-286-691-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-067-800-4
Sequence 3, Application US/09067800
Patent No. 6158024
GENERAL INFORMATION:
APPLICANT: YANOLSKY, Martin F.
TITLE: "INVENTION: Seed dispersal"
TITLE OF INVENTION: Seed dispersal
TYPE OF INVENTION: Seed dispersal
TYPE OF INVENTION: Seed dispersal
INVENTOR: Campbell, A. Flores, LLP
ADDRESS: 4700 La Villa Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/067,800
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 41,815
REFERENCE/REGISTER NUMBER: P-09 2948
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 545 9001
TELEFAX: (619) 545 8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5622 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
FEATURE:
NAME/KEY: must feature
LOCATION: 1..5622
OTHER INFORMATION:
OTHER INFORMATION: Label
OTHER INFORMATION: "Sequences as shown of the Appl. product."
US-09-067-800-4
Query Match: 4.3% Score 40.4; ID: 4; Length 5622
Post-local Similarity: 54.1% Pred. No. 0.059
Matches: 64; Conservative: 70; Indels: 0; Gaps: 0

RESULT 9
US-08 942-046-9
Sequenced 9, Application US-0894204

RESULT 10
out of 012 030 100

Pathway	1	liver
MOLECULE TYPE: DNA (genomic)		
FEATURE:		
NAME/KEY: CDS		
LOCATION: 452...1803		
OTHER INFORMATION: /Product		"cpsA"
FEATURE:		
NAME/KEY: CDS		
LOCATION: 1937...2545		
OTHER INFORMATION: /Product		"cpsB"
FEATURE:		
NAME/KEY: CDS		
LOCATION: 254...3239		
OTHER INFORMATION: /Product		"cpsC"
FEATURE:		
NAME/KEY: CDS		
LOCATION: 624...1395		
OTHER INFORMATION: /Product		"cpsD"
FEATURE:		
NAME/KEY: CDS		
LOCATION: 4051...4731		
OTHER INFORMATION: /Product		"cpsE"
FEATURE:		
NAME/KEY: CDS		
LOCATION: 4898...5854		
OTHER INFORMATION: /Product		"cpsF"
FEATURE:		
NAME/KEY: CDS		
LOCATION: 6425...7540		
OTHER INFORMATION: /Product		"cpsG"
FEATURE:		
NAME/KEY: CDS		
LOCATION: 7736...8212		
OTHER INFORMATION: /Product		"cpsH"
FEATURE:		
NAME/KEY: CDS		
LOCATION: 8221...9192		
OTHER INFORMATION: /Product		"cpsI"
FEATURE:		
NAME/KEY: CDS		
LOCATION: 9285...10364		
OTHER INFORMATION: /Product		"cpsJ"
FEATURE:		
NAME/KEY: CDS		
LOCATION: 10392...11339		
OTHER INFORMATION: /Product		"cpsK"
FEATURE:		
NAME/KEY: misc feature		
LOCATION: 11452...12222		
OTHER INFORMATION: /Product		"CDS (cps L) covered CDS"
OTHER INFORMATION: (cps K) on nucleotides 10392-11339"		
FEATURE:		
NAME/KEY: CDS		
LOCATION: 12243...13651		
OTHER INFORMATION: /Product		"cpsM"
FEATURE:		
NAME/KEY: misc feature		
LOCATION: 13742...14305		
OTHER INFORMATION: /Product		"CDS on the"
OTHER INFORMATION: comp. cons. 97.47332"		
OTHER INFORMATION: /Product		"orfZ"
FEATURE:		
NAME/KEY: terminator		
LOCATION: 246...252		
FEATURE:		
NAME/KEY: promoter		
LOCATION: 274...302		
FEATURE:		
NAME/KEY: PIS		
LOCATION: 440...445		

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Query Matched: 4.58; Score 33; DB 1; Length 14602;
Best Local Similarity 49.7%; Prod No. 12;
Matches 84; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 560 ccttcaactgaacctactatctttatgatacttatcatctttatgttaaaacatcgcg 619
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 14073 CTTCACGCTGATTAATTATAGTAAATCATGGTAATTTTAAATAAACCGAATTTTC 14014

QY 620 ataatgatgacttcagatagaagatttcgaatatccagaccatccacacatcctaac 679
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 14013 AGGCATGATACGTGAATCTTTTGACTTAATAAAAAGCAATCCYACAAACATTCAC 13964

QY 680 ctcttgaaaatgatgactctctctctcttattatgacattatctct 728
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 13953 CTGGCTAAATATATTATCTATCTTATCTTCCTTAGGAGGATTAATGATAT 13905


RESULT 13
US-08-746-682A 1/c
Sequence 1, Application: US/0874682A
Patent No. 5786184

GENERAL INFORMATION:
APPLICANT: STINGELE, Transversa
APPLICANT: MOLEY, Brad
TITLE OF INVENTION: LACTIC BACTERIA PRODUCTION
TITLE OF INVENTION: EXOGLYCOSCHARIDES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pernille & Edmunds
STREET: 1155 Avenue of The Americans
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10046

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
INTERFACING UNIT: pc t-298-i05
SOFTWARE: Patient In Repository #1.0, Version #1.0
CONNECT APPLICATION DATA:
APPLICATION NUMBER: US/08/746,682A
FILING DATE: 14-Nov-1996
CLASSIFICATION: A45

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/997,236
FILING DATE: 20-JUN-1995
APPLICATION NUMBER: EP 96201669.9
FILING DATE: 20-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Edmunds A. Allan
REGISTRATION NUMBER: 40256
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14602 base pairs
TYPE: nucleic acid
STRANDINESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURES:
NAME/KEY: CDS
LOCATION: 452..1804
OTHER INFORMATION: /product "cpsA"
FEATURE:
NAME/KEY: CDS
LOCATION: 1807..2545
OTHER INFORMATION: /product "cpsB"
FEATURE:
NAME/KEY: CDS
LOCATION: 2547..3249
OTHER INFORMATION: /product "cpsC"
FEATURE:
NAME/KEY: CDS
LOCATION: 3249..3995
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1  OTHER INFORMATION: /product "qpsd"
2  FEATURE:
3  NAME/KEY: "qpsd"
4  LOCATION: 4051..4741
5  OTHER INFORMATION: /product "qpsd"
6  FEATURE:
7  NAME/KEY: "qpsd"
8  LOCATION: 4009..5064
9  OTHER INFORMATION: /product "qpsd"
10 FEATURE:
11 NAME/KEY: "qpsd"
12 LOCATION: 6426..7540
13 OTHER INFORMATION: /product "qpsd"
14 FEATURE:
15 NAME/KEY: "qpsd"
16 LOCATION: 1700..3612
17 OTHER INFORMATION: /product "qpsd"
18 FEATURE:
19 NAME/KEY: "qpsd"
20 LOCATION: 9220..9792
21 OTHER INFORMATION: /product "qpsd"
22 FEATURE:
23 NAME/KEY: "qpsd"
24 LOCATION: 9206..10664
25 OTHER INFORMATION: /product "qpsd"
26 FEATURE:
27 NAME/KEY: "qpsd"
28 LOCATION: 10476..11339
29 OTHER INFORMATION: /product "qpsd"
30 FEATURE:
31 NAME/KEY: "qpsd"
32 LOCATION: 11020..12222
33 OTHER INFORMATION: /product "qpsd"
34 OTHER INFORMATION: (qps k) on nucleotide 10992-11339"
35 FEATURE:
36 NAME/KEY: "qpsd"
37 LOCATION: 12200..13031
38 OTHER INFORMATION: /product "qpsd"
39 FEATURE:
40 NAME/KEY: "qpsd"
41 LOCATION: 13742..14805
42 OTHER INFORMATION: /product "qpsd"
43 OTHER INFORMATION: "qpsd on the"
44 OTHER INFORMATION: "complementary strand"
45 FEATURE:
46 NAME/KEY: "qpsd"
47 LOCATION: 281..282
48 FEATURE:
49 NAME/KEY: "qpsd"
50 LOCATION: 271..302
51 FEATURE:
52 NAME/KEY: "qpsd"
53 LOCATION: 341..445
54 OTHER INFORMATION:
55 ON 750-825A:
56
57 QUERY MATCH:
58 Score: 449 DB: 1 Length: 146025
59 Host Local Similarity: 48.796 Prod. No. 166
60 Matches: 847 Observed: 92 Mismatch: 859 Indels: 02 Gaps: 02
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1  RESULT: 14
2  US-08-433-522A-7
3  Sequence 7, Application: US/08131522A
4  Patent No.: 6013514
5  GENERAL INFORMATION:
6  APPLICANT: CHROMAT, POLI
7  APPLICANT: THOMAS, WAYNE
8  APPLICANT: YANG, YAN PING
9  APPLICANT: LEONARD, SHONIA
10 APPLICANT: STEIN, DAN CHARLES
11 APPLICANT: KLEIN, MICHAEL
12 TITLE OF INVENTION: HAIR-CELLS: OTHER MEMBRANE PROTEIN
13 NUMBER OF FIGURES: 55
14 CORRESPONDENCE ADDRESS:
15 ADDRESS: SIMS, MURRAY
16 STREET: 6TH FLOOR, 440 University Avenue
17 CITY: Toronto
18 STATE: Ontario
19 COUNTRY: Canada
20 ZIP: M5G 1R7
21 COMPUTER RELEVABLE FORM:
22 MEDIUM TYPE: Floppy disk
23 COMPUTER: IBM PC compatible
24 OPERATING SYSTEM: PC DOS/MS DOS
25 SOFTWARE: Patent in Release #1.0, Version #1.23
26 CURRENT APPLICATION DATA:
27 APPLICATION NUMBER: 05/067435, 522A
28 FILING DATE: 12 SEP 1995
29 CLASSIFICATION: 435
30 ATTORNEY/AGENT INFORMATION:
31 NAME: STEWART, MICHAEL J
32 REGISTRATION NUMBER: 241973
33 FEE REFERENCE: 1-3522 NUMBER: 1038-434 MTS: 1b
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: (416) 595-1155
36 TELEFAX: (416) 595-1164
37 INFORMATION FOR SEQ ID NO: 7:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 2974 base pairs
40 TYPE: nucleic acid
41 STRANDEDNESS: single
42 TOPOLOGY: linear
43 MOLECULE TYPE: DNA (genomic)
44 FEATURE:
45 NAME/KEY: "qpsd"
46 LOCATION: 986..2761
47 US-08-433-522A-7
48
49 QUERY MATCH:
50 Score: 42.41 DB: 1 Length: 2974
51 Host Local Similarity: 48.486 Prod. No. 877
52 Matches: 902 Observed: 92 Mismatch: 962 Indels: 02 Gaps: 02
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[illegible]

C⁺ The secreted proteins and its

CC therapy. Pathological conditions can be diagnosed by determining the



GenCode version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein Protein search, using SW model

Run on: August 12, 2002, 14:54:52 ; Search time 31.1 seconds
(without alignments)
1104,595 Matches (0.11 updates/sec)

Title: US-09-825-882-8
Percent score: 409
Sequence: 1 MTEFLPIFFSSVVFVYIC
.....FISWFMQMPYWEKERISSP 309

Scoring table:
Gap: 60.0 ; Gapext: 60.0

Search: 747574 seqs, 11074796 residues

Word size: 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: listing first 45 summaries

Database:

1: US090801_0428022*
2: US090801_0428022*
3: US090801_0428022*
4: US090801_0428022*
5: US090801_0428022*
6: US090801_0428022*
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19: US090801_0428022*
20: US090801_0428022*
21: US090801_0428022*
22: US090801_0428022*

Prod. No. is the number of results produced by search to type 1
score greater than or equal to the score of the result being printed,
and is ordered by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	19.4	148	AAE03828	Human gene 11 copy
2	44	13.9	309	AAE03828	Human T2R33 amino
3	44	11.3	306	AAE03828	Human T2R33 amino
4	35	11.3	319	AAE03828	Human T2R33 amino
5	35	11.3	319	AAE03828	Human T2R33 amino
6	34	11.0	299	AAE03828	Human T2R33 amino
7	31	10.0	309	AAE03828	Human T2R33 amino
8	27	8.7	299	AAE03828	Human T2R33 amino
9	25	8.1	256	AAE03828	Human T2R33 amino
10	25	8.1	256	AAE03828	Human T2R33 amino
11	25	8.1	299	AAE03828	Human T2R33 amino

12	24	7.8	148	AAE03828	Human T2R33 amino
13	22	7.1	129	AAE03828	Human T2R33 amino
14	21	6.8	63	AAE03828	Human T2R33 amino
15	18	5.8	84	AAE03828	Human T2R33 amino
16	18	5.8	121	AAE03828	Human T2R33 amino
17	18	5.8	108	AAE03828	Human T2R33 amino
18	16	5.2	72	AAE03828	Human T2R33 amino
19	14	4.5	111	AAE03828	Human T2R33 amino
20	14	4.5	111	AAE03828	Human T2R33 amino
21	14	4.5	111	AAE03828	Human T2R33 amino
22	13	4.2	43	AAE03828	Human T2R33 amino
23	11	3.6	293	AAE03828	Human T2R33 amino
24	11	3.6	312	AAE03828	Human T2R33 amino
25	10	3.2	59	AAE03828	Human T2R33 amino
26	10	3.2	123	AAE03828	Human T2R33 amino
27	10	3.2	150	AAE03828	Human T2R33 amino
28	10	3.2	485	AAE03828	Human T2R33 amino
29	10	3.2	405	AAE03828	Human T2R33 amino
30	10	3.2	408	AAE03828	Human T2R33 amino
31	10	3.2	442	AAE03828	Human T2R33 amino
32	9	2.9	60	AAE03828	Human T2R33 amino
33	9	2.9	70	AAE03828	Human T2R33 amino
34	9	2.9	129	AAE03828	Human T2R33 amino
35	9	2.9	295	AAE03828	Human T2R33 amino
36	9	2.9	303	AAE03828	Human T2R33 amino
37	9	2.9	311	AAE03828	Human T2R33 amino
38	9	2.9	343	AAE03828	Human T2R33 amino
39	9	2.9	343	AAE03828	Human T2R33 amino
40	8	2.6	47	AAE03828	Human T2R33 amino
41	8	2.6	61	AAE03828	Human T2R33 amino
42	6	2.6	100	AAE03828	Human T2R33 amino
43	6	2.6	117	AAE03828	Human T2R33 amino
44	6	2.6	192	AAE03828	Human T2R33 amino
45	6	2.6	269	AAE03828	Human T2R33 amino

ALIGNMENTS

RESULT 1

AAE03828

US090801_0428022*

US090801_0428022*

US090801_0428022*

US090801_0428022*

US090801_0428022*

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US090801_0428022*

US090801_0428022*

XX
DB Wt: 2001-476164/51.
DB N PDB: AHH9984.
XX
PI Isolated polypeptide for treatment of diseases, diagnostics, raising
PI antibodies and research use.
XX
PS Claim 20: Page 1202: 1275pp: English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC for instance, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention.
XX
SQ Sequence 84 AA:

Query Match 5.88; Score 18; DB 22; Length 84;
Best Local Similarity 100.08; Pred. No. 4.4e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 214 KGSQPSIKVHKAQTV 231
DB 6 KGSQPSIKVHKAQTV 23

Search completed: August 12, 2002, 13:59:25
Job time: 273 sec

protein and nucleic acids are also useful as food supplements. The present sequence encodes a secreted protein of the invention.

Sequence 2695 BP: 858 At 427 C; 486 G; 919 T; 5 others.

Query Match: 74.5%; Score 692.6; E: 2.2; Length: 2695;

Host: Local Similarity: 84.6%; Prod. No. 2.86-181;

Matches: 769; Conservation: 1; Mismatches: 149; Indels: 2; Gaps: 1;

```

UY 1 atataacttttaccacatttttccactctctactgattacatttatataga 60
Db 1129 atataacttttaccacatttttccactctctactgattacatttatataga 1198
UY 41 attttctctactctctactgatttatatatttatatttatatttataga 120
Db 1189 attttctctactctctactgatttatatatttatatttatatttataga 1248
UY 121 atctctctactgattacattctctactgattctctactgattctctactg 180
Db 1249 atctctctactgattacattctctactgattctctactgattctctactg 1368
UY 181 atattatttttatactgatttatactgatttatactgatttatactgatt 240
Db 1409 atattatttttatactgatttatactgatttatactgatttatactgatt 1368
UY 241 atataacttttaccacatttttccactctctactgattacatttatataga 300
Db 1469 atataacttttaccacatttttccactctctactgattacatttatataga 1428
UY 401 atataacttttaccacatttttccactctctactgattacatttatataga 360
Db 1429 atataacttttaccacatttttccactctctactgattacatttatataga 1488
UY 461 ttaaaatgattgatttatactgatttatactgatttatactgatttatactg 420
Db 1489 ttaaaatgattgatttatactgatttatactgatttatactgatttatactg 1548
UY 421 atctctctactgattacattctctactgattctctactgattctctactg 480
Db 1549 atctctctactgattacattctctactgattctctactgattctctactg 1608
UY 481 atataacttttaccacatttttccactctctactgattacatttatataga 540
Db 1609 atataacttttaccacatttttccactctctactgattacatttatataga 1668
UY 541 atataacttttaccacatttttccactctctactgattacatttatataga 600
Db 1669 atataacttttaccacatttttccactctctactgattacatttatataga 1728
UY 601 atctctctactgattacattctctactgattctctactgattctctactg 660
Db 1729 atctctctactgattacattctctactgattctctactgattctctactg 1788
UY 661 atctctctactgattacattctctactgattctctactgattctctactg 720
Db 1789 atctctctactgattacattctctactgattctctactgattctctactg 1848
UY 721 atctctctactgattacattctctactgattctctactgattctctactg 777
Db 1849 atctctctactgattacattctctactgattctctactgattctctactg 1908
UY 778 atctctctactgattacattctctactgattctctactgattctctactg 837
Db 1909 atctctctactgattacattctctactgattctctactgattctctactg 1968
UY 838 atctctctactgattacattctctactgattctctactgattctctactg 897
Db 1969 atctctctactgattacattctctactgattctctactgattctctactg 2028
UY 898 atctctctactgattacattctctactgattctctactgattctctactg 940
Db 2029 atctctctactgattacattctctactgattctctactgattctctactg 2088

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RESULT 12

ABAY0967

ABAY0967 standard; cDNA; 2695 BP.

XX

AC ABAY0967;

XX 14-FEB-2002 (first entry)

XX

DE Human polynucleotide SEQ ID NO 183.

XX

XX Human; clone: K4305-7; clone y08-1; ATCC number 98599; gene therapy;

KW immune disorder; bacterial infection; fungal infection; cancer; tumor;

KW autoimmune disorder; systemic lupus erythematosus; wound; ulcers; inhibin;

KW osteoporosis; osteoarthritis; nervous system disorder; neuropathy;

KW Alzheimer's disease; Parkinson's disease; Huntington's disease; arthritis;

KW hemophilia; varicella; streptococcal sepsis; orthopedic surgery;

KW ischemia; reperfusion injury; inflammatory bowel disease; chemotherapy;

KW Crohn's disease; cytotoxic anti-inflammatory immunomodulatory;

KW neuroprotective; haemostatic; thrombolytic; anti-inflammatory; ss.

XX Homo sapiens.

OS

PN US2001049345-A1.

XX

XX 08-MAY-2001.

XX

PE C4-DEC-2000; 200005-0729674.

XX

PE 10-APR-1997; 9705-126425P.

PR 04-DEC-1997; 9705-067454P.

PR 20-DEC-1997; 9705-068479P.

PR 02-JAN-1998; 9805-070446P.

PR 07-JAN-1998; 9805-070643P.

PR 08-JAN-1998; 9805-070755P.

PR 11-JAN-1998; 9805-071404P.

PR 22-JAN-1998; 9805-072184P.

PR 40-JAN-1998; 9805-073095P.

PR 18-FEB-1998; 9805-075048P.

PR 30-MAR-2000; 200005-0549430.

PR 23-NOV-1998; 9805-0197886.

XX

PA (JACO/) JACOBS K.

PA (MCO/) MCOY J M.

PA (LAV/) LAVALLIE E R.

PA (COL/) COLLINS-KACIE L A.

PA (EVAN/) EVANS G.

PA (MERK/) MERKLE D.

PA (TRIA/) TRIANEY M.

PA (JACO/) JACOBSON M J.

PA (STEI/) STEININGER R J.

PA (SPAU/) SPAULDING V.

PA (WONG/) WONG G G.

PA (CLAG/) CLAGG H.

PA (FERH/) FERRELL K.

XX

P1 Jacobs K, MCOY JM, LAVALLIE ER, COLLINS-Kacie LA, Evans G,

P1 Morberg D, Treacy M, Aoshino M, Steininger RJ, Spaulding V,

P1 Wong GG, Clark H, Ferrell K;

XX W01: 2002 04/25/05.

DE P-PSDB: AB855789.

XX

XX New secreted proteins and encoding polynucleotides, useful in gene

PT therapies, particularly for preventing or treating autoimmune

PT disorders, cancer, graft-versus-host disease, wound, osteoporosis,

PT stroke or inflammation.

XX

PS Disclosure: Page 420-421; 44pp; English.

XX

CC The invention relates to isolated polynucleotides (ABAY0967, ABAY0968) and

CC ABAY0980) and encoded proteins (AB855698-AB855800), especially

[illegible][illegible][illegible]

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UY 480 aacttaacttgaataatcaaattgaataatgcaatgatacttttcaaatataactatagcc 540
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
IB 481 aacttaacttgaataatcaaatgaaatgcaatgcaacttcccaacttgaactatagcc 540
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
UY 541 atgataatgaacttgaacttgaacttgaacttgaacttgaacttgaacttgaacttgaact 600
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
IB 541 atgataatgaacttgaacttgaacttgaacttgaacttgaacttgaacttgaacttgaact 600
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
UY 601 tcttttgaatgaacttgaacttgaacttgaacttgaacttgaacttgaacttgaact 660
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
IB 601 tcttttgaatgaacttgaacttgaacttgaacttgaacttgaacttgaacttgaact 660
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
UY 661 aacttaacttgaataatcaaattgaataatgcaatgatacttttcaaatataactatagcc 720
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
IB 661 aacttaacttgaataatcaaattgaataatgcaatgatacttttcaaatataactatagcc 720
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
UY 721 tacttttgaacttaataatcaaatgaaatgcaatgcaacttcccaacttgaactatagcc 780
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
IB 721 tacttttgaacttaataatcaaatgaaatgcaatgcaacttcccaacttgaactatagcc 780
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
UY 781 tcaatgatacttgaacttgaacttgaacttgaacttgaacttgaacttgaacttgaact 840
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
IB 781 tcaatgatacttgaacttgaacttgaacttgaacttgaacttgaacttgaacttgaact 840
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
UY 841 tgaataatgaataatcaaatgaaatgcaatgatacttttcaaatataactatagcc 900
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
IB 841 tgaataatgaataatcaaatgaaatgcaatgatacttttcaaatataactatagcc 900
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
UY 901 atgaataatgaataatcaaatgaaatgcaatgatacttttcaaatataactatagcc 930
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
IB 901 atgaataatgaataatcaaatgaaatgcaatgatacttttcaaatataactatagcc 930
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Search completed: August 12, 2002, 12:43:26
Job Time: 3908 sec

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Sequentia: 981 BP; 250 A, 177 c; 179 d; 419 f; 0 calibr.

Journal of the American Statistical Association

[illegible]

AA1198196

AA198196;

XX
DT
12-Oct-2001 (first entry)

Human EST-derived coding sequence SIO ID NO: 534

XX Human: slab over roof, front fly, vest, hamst over me, over horse

KW
tomato of Bonkey; doff seed uphlin exposed sequence 1447 FSL

biologically; gene therapy; nutrition; SS

XX
OS Homo sapiens.

XX
W0200154477 A2
LN

01-416-3001

XX
1002-8000-30
14

PP 25 JAN-2001; 2001W10502587
XX

PR 25-JAN-2000; 2000US 0491404.
PR 17-JUL-2000; 2000US 0617746.

PR	03-ADD-2000;	21100US	0641451
PR	15-ETB-2000;	2000US	0663870

XX

XX (1951) 115-116

21 Taroq YF, Liu C, Zhou F, Q
22
23 Cao Y, Bernard KA, Zhang S

WPI: 2001-476164/51

10K P-PS103; AAM23547.

Isolated polypeptides for re-

XX and bodies and research use

PS Claim 1; Page 27: 1.77pp; P
XX

Elbow present in front of provice

cow, pig, hamster, monkey, mouse, rabbit, rat, snake, squirrel, turtle, and various birds.

From the organization of interest

of forensics, gene mapping, and biodiversity and for mutation

CC of the invention.

Sequentia: 1. 200 Mi. 6' 11" 200'


```

D1 16-MAY-2001 (first entry)
XX Human T2R37 nucleotide sequence SFG ID NO:64
XX
XX Human: rat: mouse: T2R: taste receptor: G-protein coupled receptor:
XX taste transduction G-protein coupled receptor: identification: tongue:
XX taste sensory neuron: taste cell: taste modulator: food:
XX taste signalling pathway: ds.
XX
XX Homo sapiens.
XX
XX W0200118050-A2.
XX
XX 15-MAR-2001.
XX
XX 08-SEP-2000: 2000W0-US24821.
XX
XX 10-SEP-1999: 9908-0393634.
XX 22-FEB-2000: 2000US-0510332.
XX
XX (RSC) ) UNIV CALIF-POMONA.
XX (USSH) ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Zaker CS, Adler JE, Pyda N, Mueller K, Heen M;
XX WPI: 2001-211396/21.
XX P-PSDB: AAB87767.
XX
XX Nucleic acids encoding the T2R family of G-protein coupled taste
XX receptors, useful for identifying taste modulators that can be used in
XX food and pharmaceutical industries to customize taste, for e.g., to
XX decrease the bitter taste of food -
XX
XX Disclosure: Page 185: 249pp: English.
XX
XX AAF92502 to AAF92572 represent nucleic acids which encode taste
XX transduction G-protein coupled receptors designated T2R proteins
XX AAB87731 to AAB87824 represent T2R proteins, and AAB87825 to AAB87830
XX represent T2R family consensus sequences from the present invention.
XX The T2R proteins are taste modulators. The nucleic acids are useful as
XX probes for the identification of taste cells, as the nucleic acids are
XX specifically expressed in taste cells. They also serve as tools for the
XX generation of taste topographic maps that elucidate the relationship
XX between the taste cells of the tongue and taste sensory neurons leading
XX to taste centres in the brain. The taste modulators are useful for
XX pharmacological and genetic modulation of taste signalling pathways.
XX Modulatory compounds comprising T2R proteins can therefore be used in
XX food and pharmaceutical industries to customize taste, for e.g., to
XX decrease the bitter taste of food or drugs.
XX
XX Sequence 960 BP: 254 A; 178 C; 181 G; 317 T; 0 other:
XX
XX Query Match: 5.98; Score 55; DB 22; Length 960;
XX Best Local Similarity 100.0%; Pred. No. 1,20-16;
XX Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 640 aaagatctcaagatccagacgaagatccacataaagctttcgaacttga 694
XX ||||||||||||||||||||||||||||||||||||||||||||||||
XX 640 aaagatctcaagatccagacgaagatccacataaagctttcgaacttga 694
XX
XX RESULT 14
XX AAF92524
XX ID AAF92523 standard; DNA: 960 BP.
XX
XX AC AAF92523;
XX
XX 16-MAY-2001 (first entry)
XX
XX Human T2R30 nucleotide sequence SFG ID NO:52.
XX
XX Human: rat: mouse: T2R: taste receptor: G-protein coupled receptor:

```

```

XX taste transduction G-protein coupled receptor: identification: tongue;
XX taste sensory neuron; taste cell; taste modulator; food;
XX taste signalling pathway: ds.
XX
XX Homo sapiens.
XX
XX W0200118050-A2.
XX
XX 15-MAR-2001.
XX
XX 08-SEP-2000: 2000W0-US24821.
XX
XX 10-SEP-1999: 9908-0393634.
XX 22-FEB-2000: 2000US-0510332.
XX
XX (RSC) ) UNIV CALIF-POMONA.
XX (USSH) ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Zaker CS, Adler JE, Pyda N, Mueller K, Heen M;
XX WPI: 2001-211396/21.
XX P-PSDB: AAB87760.
XX
XX Nucleic acids encoding the T2R family of G-protein coupled taste
XX receptors, useful for identifying taste modulators that can be used in
XX food and pharmaceutical industries to customize taste, for e.g., to
XX decrease the bitter taste of food -
XX
XX Disclosure: Page 180-181: 249pp: English.
XX
XX AAF92502 to AAF92572 represent nucleic acids which encode taste
XX transduction G-protein coupled receptors designated T2R proteins.
XX AAB87731 to AAB87824 represent T2R proteins, and AAB87825 to AAB87830
XX represent T2R family consensus sequences from the present invention.
XX The T2R proteins are taste modulators. The nucleic acids are useful as
XX probes for the identification of taste cells, as the nucleic acids are
XX specifically expressed in taste cells. They also serve as tools for the
XX generation of taste topographic maps that elucidate the relationship
XX between the taste cells of the tongue and taste sensory neurons leading
XX to taste centres in the brain. The taste modulators are useful for
XX pharmacological and genetic modulation of taste signalling pathways.
XX Modulatory compounds comprising T2R proteins can therefore be used in
XX food and pharmaceutical industries to customize taste, for e.g., to
XX decrease the bitter taste of food or drugs.
XX
XX Sequence 960 BP: 256 A; 197 C; 183 G; 324 T; 0 other:
XX
XX Query Match: 5.98; Score 55; DB 22; Length 960;
XX Best Local Similarity 100.0%; Pred. No. 1,20-16;
XX Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 640 aaagatctcaagatccagacgaagatccacataaagctttcgaacttga 694
XX ||||||||||||||||||||||||||||||||||||||||||||||||
XX 640 aaagatctcaagatccagacgaagatccacataaagctttcgaacttga 694
XX
XX RESULT 15
XX AAF92515
XX ID AAF92515 standard; DNA: 903 BP.
XX
XX AC AAF92515;
XX
XX 16-MAY-2001 (first entry)
XX
XX Human T2R15 nucleotide sequence SFG ID NO:29.
XX
XX Human: rat: mouse: T2R: taste receptor: G-protein coupled receptor:
XX taste transduction G-protein coupled receptor: identification: tongue;
XX taste sensory neuron; taste cell; taste modulator; food;
XX taste signalling pathway: ds.
XX
XX Homo sapiens.
XX

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1. Math 2. Math 3. Math

100 811 2000 W 115.24821

[illegible]

XX

(1958) THE LEFT HEALING & HUMAN SERVICES

[illegible]
$$W(\mathbf{1}, \mathbf{1}, \mathbf{1}, \mathbf{1}, \mathbf{1}, \mathbf{1}) = 24 \left(\frac{1}{2} \right)^6 = \frac{3}{2}.$$
[illegible]

Category	Item	Value
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	1.3	1.3
	1.4	1.4
	1.5	1.5
	1.6	1.6
	1.7	1.7
	1.8	1.8
	1.9	1.9
	1.10	1.10
A.2	2.1	2.1
	2.2	2.2
	2.3	2.3
	2.4	2.4
	2.5	2.5
	2.6	2.6
	2.7	2.7
	2.8	2.8
	2.9	2.9
	2.10	2.10
A.3	3.1	3.1
	3.2	3.2
	3.3	3.3
	3.4	3.4
	3.5	3.5
	3.6	3.6
	3.7	3.7
	3.8	3.8
	3.9	3.9
	3.10	3.10
A.4	4.1	4.1
	4.2	4.2
	4.3	4.3
	4.4	4.4
	4.5	4.5
	4.6	4.6
	4.7	4.7
	4.8	4.8
	4.9	4.9
	4.10	4.10
A.5	5.1	5.1
	5.2	5.2
	5.3	5.3
	5.4	5.4
	5.5	5.5
	5.6	5.6
	5.7	5.7
	5.8	5.8
	5.9	5.9
	5.10	5.10
A.6	6.1	6.1
	6.2	6.2
	6.3	6.3
	6.4	6.4
	6.5	6.5
	6.6	6.6
	6.7	6.7
	6.8	6.8
	6.9	6.9
	6.10	6.10
A.7	7.1	7.1
	7.2	7.2
	7.3	7.3
	7.4	7.4
	7.5	7.5
	7.6	7.6
	7.7	7.7
	7.8	7.8
	7.9	7.9
	7.10	7.10
A.8	8.1	8.1
	8.2	8.2
	8.3	8.3
	8.4	8.4
	8.5	8.5
	8.6	8.6
	8.7	8.7
	8.8	8.8
	8.9	8.9
	8.10	8.10
A.9	9.1	9.1
	9.2	9.2
	9.3	9.3
	9.4	9.4
	9.5	9.5
	9.6	9.6
	9.7	9.7
	9.8	9.8
	9.9	9.9
	9.10	9.10
A.10	10.1	10.1
	10.2	10.2
	10.3	10.3
	10.4	10.4
	10.5	10.5
	10.6	10.6
	10.7	10.7
	10.8	10.8
	10.9	10.9
	10.10	10.10

[illegible]

$\frac{1}{\sqrt{\pi}} \int_{-\infty}^{\infty} f(x) e^{-x^2} dx = \frac{1}{\sqrt{\pi}} \int_{-\infty}^{\infty} f(x) e^{-x^2} dx$

of Mn^{2+} to $\text{Mn}^{3+}/2$ represent nucleic acids which encode faster translation of protein-coupled receptors displayed LTR poliovirus.

AAH8784 to AAH8784 represent L26 proteins, and AAH8785 to AAH8786 represent L28 family consensus sequences from the present invention.

The LRP proteins are taste modulators. The nucleic acids are useful as probes for the identification of taste cells, as the nucleic acids are

are specifically expressed in taste cells. They also serve as tools for the generation of taste topographic maps that elucidate the relationship

between the taste cells of the tongue and taste sensory neurons leading to taste centres in the brain. The taste modulators are useful for

pharmacological and genetic modulation of taste signalling pathways. Modulatory compounds comprising ELK proteins can therefore be used in

Food and pharmaceutical industries to customise taste, for e.g. to decrease the bitter taste of food or drugs.

XX	XX
50-40-10-0	00-40-10-0
178 °C	178 °C
41.7 °C	41.7 °C
0.0100	0.0100

2007, M. Th. 9, 36; Series 49; PB 22; Length 900;
Post 2004, Stamp 1177; Prod. No. 9, 36, 14;

[illegible][illegible]

1. *Chlorophyll a* (Chl *a*)

Characterization of Λ -modules and Λ -lattices

[illegible]

Genome version 4.5
Copyright (c) 1993 - 2000 CompuLink Ltd.

00M protein - protein search, using sw model

Run on: August 12, 2002, 13:13:14 ; Search time 43.83 seconds
(without alignments)
677.427 Million cell updates/sec

Title: US-09-825-882-8

Sequence: 1 MTEPLPLESSLVVTFVIG.....FLSWKQMGMYWCKEKTSSP 309

Scoring table:

Gapop 10.0 ; Gapext 0.5

Scorched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 88
Maximum Match 1008
Listing first 45 summaries

Database:

1: PIR_71:.*
2: PIR1:.*
3: PIR2:.*
4: PIR3:.*

Prod. No. is the number of results produced by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY:

Result No.	Score	Query Match	Length DB	ID	Description
1	130.5	8.2	341	2	hypothetical protein
2	130.5	8.2	380	2	anionotensin recept
3	126.5	7.3	387	2	conserved hypot
4	123	7.2	363	2	conserved hypot
5	120.5	7.6	441	2	conserved hypot
6	117	7.3	463	2	conserved hypot
7	116.5	7.3	416	2	hypothetical prote
8	115.5	7.2	364	2	anionotensin II rec
9	115	7.2	311	2	pharmacore receptor
10	115	7.2	358	2	ubiquitinol-cytor
11	114.5	7.2	625	2	hypothetical prote
12	112.5	7.0	412	2	oligactyl recept
13	112	7.0	355	2	hypothetical prote
14	112	7.0	1898	2	hypothetical prote
15	111.5	7.0	363	2	anionotensin II rec
16	111.5	7.0	505	2	anionotensin II rec
17	111	7.0	349	2	protein F21D12.3
18	110.5	6.9	339	2	hypothetical prote
19	110.5	6.9	363	2	hypothetical prote
20	110.5	6.9	366	2	anionotensin II rec
21	110.5	6.9	548	2	hypothetical prote
22	109	6.8	432	2	hypothetical prote
23	108.5	6.8	387	2	hypothetical prote
24	108.5	6.8	406	2	serotonin 4 recept
25	108.5	6.8	770	2	hypothetical prote
26	108	6.8	380	2	hypothetical prote
27	107.5	6.7	317	2	hypothetical prote
28	107.5	6.7	339	2	hypothetical prote
29	106.5	6.7	268	2	hypothetical prote

30	106.5	6.7	352	2	neuropeptide Y/pep
31	106.5	6.7	359	2	anionotensin II rec
32	106.5	6.7	906	2	uncharacterized re
33	106	6.6	328	2	odorant receptor 8
34	106	6.6	380	2	kappa opioid recep
35	106	6.6	380	2	kappa opioid recep
36	106	6.6	707	2	hypothetical prote
37	105.5	6.6	274	2	protein F41D10.8
38	105.5	6.6	359	2	anionotensin II rec
39	105	6.6	310	2	hypothetical prote
40	105	6.6	380	2	kappa opioid recep
41	105	6.6	497	2	MAOI dehydrogenase
42	104.5	6.5	355	2	G protein coupled
43	104.5	6.5	488	2	hypothetical prote
44	104.5	6.5	477	2	hypothetical prote
45	104	6.5	352	2	tusin (LSTRA)

ALIGNMENTS

RESULT 1	126920	hypothetical protein Y45P108.6 - Caenorhabditis elegans	
C1Species:	Caenorhabditis elegans		
C1Date:	15 Oct 1999	Sequence revision 15 Oct 1999	Final change 21 Jul 2000
C1Accession:	126920		
Reference:	A.	Submitted to the EMBL data library, January 1998	
A1Reference number:	220286		
A1Accession:	126920		
A1Status:	Preliminary	Translated from GR/EMBL/DBD	
A1Molecule type:	DNA		
A1Residues:	1-341	(SIL)	
A1Cross reference:	EMBL:AL021487; JIDN:CAAL6458.1; GSPDB:G080022; CESP:Y45P108.6		
A1Experimental source:	clone Y45P108		
A1Genetics:			
A1Gene:	CESP:Y45P108.6		
A1Map position:	4		
A1Date:	1999		
C1Superfamily:	Caenorhabditis elegans	hypothetical protein C1AAL2.9b	
Query Match	8.2%	Score 130.5; DB 2; Length 341;	
Best Local Similarity	22.1%	Prod. No. 0.0023	
Matches	71	Conservative 54; Mismatches 86; Indels 111; Gaps 20;	
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REFULOT, L.

62. LILLYWISTENHAFEN ALTERNATIVE TREATMENT FOR SOME AT-RISK YOUNG MEN, PUBL. 1-20-07

DB 1061 ENINSTRKIVSRQGLFHSQYTRHSFSTKQMSLHHLLGLYAWAPWNRKQSLND 1120
 A:Reference number: 221815
 A:Accession: 139109
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1,1888 (GEN)
 A:Cross-reference: EMBL/208543, FJ087461/1964, 135938, G000066, S008, S009, 12, 026
 A:Experimental source: strain 9726; cosmid 60812
 C:Genotes:
 A:Gene: SPB:SPB/6012/620
 A:Map position: 1
 C:Superfamily: Schizosaccharomyces hypodermal protein SPA/612/620

DB 1062 ENINSTRKIVSRQGLFHSQYTRHSFSTKQMSLHHLLGLYAWAPWNRKQSLND 1120
 A:Reference number: 221815
 A:Accession: 139109
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1,1888 (GEN)
 A:Cross-reference: EMBL/208543, FJ087461/1964, 135938, G000066, S008, S009, 12, 026
 A:Experimental source: strain 9726; cosmid 60812
 C:Genotes:
 A:Gene: SPB:SPB/6012/620
 A:Map position: 1
 C:Superfamily: Schizosaccharomyces hypodermal protein SPA/612/620

DB 1063 ENINSTRKIVSRQGLFHSQYTRHSFSTKQMSLHHLLGLYAWAPWNRKQSLND 1120
 A:Reference number: 221815
 A:Accession: 139109
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1,1888 (GEN)
 A:Cross-reference: EMBL/208543, FJ087461/1964, 135938, G000066, S008, S009, 12, 026
 A:Experimental source: strain 9726; cosmid 60812
 C:Genotes:
 A:Gene: SPB:SPB/6012/620
 A:Map position: 1
 C:Superfamily: Schizosaccharomyces hypodermal protein SPA/612/620

RESULT 14

hypodermal protein SPA/612/620 - function: protein (66 bits, 100% identity, 100% positive, 100% negative, 100% conserved)

Query Match: 7.08; Score: 112; DB: 2; Length: 655;
 Best local similarity: 24.76; Pos: 0.076; Neg: 0.076; Mismatches: 88; Indels: 90; Gaps: 16;

DB 1061 ENINSTRKIVSRQGLFHSQYTRHSFSTKQMSLHHLLGLYAWAPWNRKQSLND 1120
 A:Reference number: 221815
 A:Accession: 139109
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1,1888 (GEN)
 A:Cross-reference: EMBL/208543, FJ087461/1964, 135938, G000066, S008, S009, 12, 026
 A:Experimental source: strain 9726; cosmid 60812
 C:Genotes:
 A:Gene: SPB:SPB/6012/620
 A:Map position: 1
 C:Superfamily: Schizosaccharomyces hypodermal protein SPA/612/620

DB 1062 ENINSTRKIVSRQGLFHSQYTRHSFSTKQMSLHHLLGLYAWAPWNRKQSLND 1120
 A:Reference number: 221815
 A:Accession: 139109
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1,1888 (GEN)
 A:Cross-reference: EMBL/208543, FJ087461/1964, 135938, G000066, S008, S009, 12, 026
 A:Experimental source: strain 9726; cosmid 60812
 C:Genotes:
 A:Gene: SPB:SPB/6012/620
 A:Map position: 1
 C:Superfamily: Schizosaccharomyces hypodermal protein SPA/612/620

DB 1063 ENINSTRKIVSRQGLFHSQYTRHSFSTKQMSLHHLLGLYAWAPWNRKQSLND 1120
 A:Reference number: 221815
 A:Accession: 139109
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1,1888 (GEN)
 A:Cross-reference: EMBL/208543, FJ087461/1964, 135938, G000066, S008, S009, 12, 026
 A:Experimental source: strain 9726; cosmid 60812
 C:Genotes:
 A:Gene: SPB:SPB/6012/620
 A:Map position: 1
 C:Superfamily: Schizosaccharomyces hypodermal protein SPA/612/620

RESULT 15

hypodermal protein SPA/612/620 - function: protein (66 bits, 100% identity, 100% positive, 100% negative, 100% conserved)

Query Match: 7.08; Score: 112; DB: 2; Length: 655;
 Best local similarity: 24.76; Pos: 0.076; Neg: 0.076; Mismatches: 88; Indels: 90; Gaps: 16;

DB 1061 ENINSTRKIVSRQGLFHSQYTRHSFSTKQMSLHHLLGLYAWAPWNRKQSLND 1120
 A:Reference number: 221815
 A:Accession: 139109
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1,1888 (GEN)
 A:Cross-reference: EMBL/208543, FJ087461/1964, 135938, G000066, S008, S009, 12, 026
 A:Experimental source: strain 9726; cosmid 60812
 C:Genotes:
 A:Gene: SPB:SPB/6012/620
 A:Map position: 1
 C:Superfamily: Schizosaccharomyces hypodermal protein SPA/612/620

Reported: S. J. Chatterjee, C. M. J. Barrett, R. G. Rajandream, M. A. Wood, V. submitted to the EMBL Data Library, August 1995

A:Reference number: 221815
 A:Accession: 139109
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1,1888 (GEN)
 A:Cross-reference: EMBL/208543, FJ087461/1964, 135938, G000066, S008, S009, 12, 026
 A:Experimental source: strain 9726; cosmid 60812
 C:Genotes:
 A:Gene: SPB:SPB/6012/620
 A:Map position: 1
 C:Superfamily: Schizosaccharomyces hypodermal protein SPA/612/620

Query Match: 7.08; Score: 112; DB: 2; Length: 655;
 Best local similarity: 24.76; Pos: 0.076; Neg: 0.076; Mismatches: 88; Indels: 90; Gaps: 16;

DB 1061 ENINSTRKIVSRQGLFHSQYTRHSFSTKQMSLHHLLGLYAWAPWNRKQSLND 1120
 A:Reference number: 221815
 A:Accession: 139109
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1,1888 (GEN)
 A:Cross-reference: EMBL/208543, FJ087461/1964, 135938, G000066, S008, S009, 12, 026
 A:Experimental source: strain 9726; cosmid 60812
 C:Genotes:
 A:Gene: SPB:SPB/6012/620
 A:Map position: 1
 C:Superfamily: Schizosaccharomyces hypodermal protein SPA/612/620

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 A:Reference number: 221815
 A:Accession: 139109
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1,1888 (GEN)
 A:Cross-reference: EMBL/208543, FJ087461/1964, 135938, G000066, S008, S009, 12, 026
 A:Experimental source: strain 9726; cosmid 60812
 C:Genotes:
 A:Gene: SPB:SPB/6012/620
 A:Map position: 1
 C:Superfamily: Schizosaccharomyces hypodermal protein SPA/612/620

DB 1063 ENINSTRKIVSRQGLFHSQYTRHSFSTKQMSLHHLLGLYAWAPWNRKQSLND 1120
 A:Reference number: 221815
 A:Accession: 139109
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1,1888 (GEN)
 A:Cross-reference: EMBL/208543, FJ087461/1964, 135938, G000066, S008, S009, 12, 026
 A:Experimental source: strain 9726; cosmid 60812
 C:Genotes:
 A:Gene: SPB:SPB/6012/620
 A:Map position: 1
 C:Superfamily: Schizosaccharomyces hypodermal protein SPA/612/620

RESULT 15

hypodermal protein SPA/612/620 - function: protein (66 bits, 100% identity, 100% positive, 100% negative, 100% conserved)

Query Match: 7.08; Score: 112; DB: 2; Length: 655;
 Best local similarity: 24.76; Pos: 0.076; Neg: 0.076; Mismatches: 88; Indels: 90; Gaps: 16;

DB 1061 ENINSTRKIVSRQGLFHSQYTRHSFSTKQMSLHHLLGLYAWAPWNRKQSLND 1120
 A:Reference number: 221815
 A:Accession: 139109
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1,1888 (GEN)
 A:Cross-reference: EMBL/208543, FJ087461/1964, 135938, G000066, S008, S009, 12, 026
 A:Experimental source: strain 9726; cosmid 60812
 C:Genotes:
 A:Gene: SPB:SPB/6012/620
 A:Map position: 1
 C:Superfamily: Schizosaccharomyces hypodermal protein SPA/612/620

DB 1062 ENINSTRKIVSRQGLFHSQYTRHSFSTKQMSLHHLLGLYAWAPWNRKQSLND 1120
 A:Reference number: 221815
 A:Accession: 139109
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1,1888 (GEN)
 A:Cross-reference: EMBL/208543, FJ087461/1964, 135938, G000066, S008, S009, 12, 026
 A:Experimental source: strain 9726; cosmid 60812
 C:Genotes:
 A:Gene: SPB:SPB/6012/620
 A:Map position: 1
 C:Superfamily: Schizosaccharomyces hypodermal protein SPA/612/620

DB 1063 ENINSTRKIVSRQGLFHSQYTRHSFSTKQMSLHHLLGLYAWAPWNRKQSLND 1120
 A:Reference number: 221815
 A:Accession: 139109
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1,1888 (GEN)
 A:Cross-reference: EMBL/208543, FJ087461/1964, 135938, G000066, S008, S009, 12, 026
 A:Experimental source: strain 9726; cosmid 60812
 C:Genotes:
 A:Gene: SPB:SPB/6012/620
 A:Map position: 1
 C:Superfamily: Schizosaccharomyces hypodermal protein SPA/612/620

Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
 F346-73/omaliu: transmembrane #status predicted <TM>
 F261-102/omaliu: transmembrane #status predicted <TM>
 F2120-140/omaliu: transmembrane #status predicted <TM>
 F2161-179/omaliu: transmembrane #status predicted <TM>
 F2209-244/omaliu: transmembrane #status predicted <TM>
 F2257-278/omaliu: transmembrane #status predicted <TM>
 F2260-313/omaliu: transmembrane #status predicted <TM>
 F2413-2429/43/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F279-152/438/453/534/Binding site: phosphate (Asn) (covalent) #status predicted
 F346/Binding site: phosphate (Ile) (covalent) #status predicted

Query Match 7.08; Score 111.5; DH 2; Length 463;

Best Local Similarity 20.78; Pred. No. 0.087;

Matches 69; Conservative 65; Mismatches 142; Indels 67; Gaps 17;

```

QY 5 LPTTFSSIVVTFVGNFANCFAL-----VNSTFWEKPGQISFALQITLALAV 53
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QD 47 LPVLY---YMLFVIG-FAVNIWVVSLECGQKPKKVSITYF---NLALADLLATLP 98
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 54 SSVLLIWLILNW-YSTVLNPAFNSVEVRTATVNIWAVINHFSNWLATISIFL--LKI 110
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
QD 99 -----LMAIVYSYRYDMLFGP-----VMCKVPGSFLILNMFA-----SIFPITQMSY 140
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 111 ANFSNPTFLHLKRYKVS-----VILVMLGPIILFLAGHLFVILNMNEIVRKEFGNMIV 164
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
QD 141 DRVQSVITPPLSQRNPWQASVVPVWCMAGLSLPTPF-----KDVRTIFYLQVNG 195
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 165 KIKTRSAWYS-NMIVTVANVVPPIILISFELLISLCHLRFWQIQRK--SQPST 221
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
QD 196 LMAFFERFYAAMSAITAMNLSPTIFPIETAVCPGLEHLEINSYCKNPITPQVL 255
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 222 KVHIAIQTIVSPTICATVF--LSIMSWSRGSLFNKPEVM-----ECKAIRSPY 272
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
QD 256 KM--AAAVVLAFLITWLPPIVLTPLDALWGGIINSCEVLAVIDLALPPALIDPTNS 311
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 273 STIRPILLWNRKELKGLTISVFWCMRYWVAGLN 305
      : : : : : : : : : : : : : : : : : : : : : : : : : : :
QD 312 VNRPITVGVNRRQGRKRSVRFVPTIWLQGR 344
      : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Search completed: August 12, 2002, 14:51:10
 Job time: 2.76 sec

C/Spectra: Mus musculus (house mouse)
 C/Dates: 08-May-1995 *sequence_revision 21 Jul 1995 *text_change 21 Jan 2000
 C/Accession: S52448
 R/Editor: J. Kraehenbuhl, J.P.
 Submitted to the EMBL data library: November 1994
 Address: F.115, Str. 21, Institut de la Recherche chain reaction of rearranged and
 A/Reference number: S52445
 A/Accession: S52448
 A/Status: preliminary
 A/Molecule type: tNA
 A/Residues: 1-128 SHER
 A/Cross-references: EMBL:382689
 C/Comment:
 A/Feature: 14/1
 C/Superfamily: immunoglobulin V region; immunoglobulin hamology
 C/Keywords: heterotrimer; immunoglobulin
 F/37-115/Domains: immunoglobulin hamology <IMM>

Query Match 2.48; Score 7; DB 2; Length 128;
 Best Local Similarity 100.0%; Prod. No. 45;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 L1WILL 64
 |||||
 DB 7 L1WILL 13

RESULT 8
 J10073
 aberrant kappa transcript - mouse
 C/Spectra: Mus musculus (house mouse)
 C/Dates: 04-Sep-1998 *sequence_revision 04-Sep-1998 *text_change 21-Jan-2000
 C/Accession: J10073
 R/Editor: W. L. Mendel, E. J. Levy, S.
 M.O.I.: Immunol., 25, 991-995, 1988
 A/Title: H3H3H3 fusion cell lines contain an aberrant kappa transcript.
 A/Reference number: J10073; M010-89112246
 A/Accession: J10073
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-128 <AB>
 A/Cross-references: DB:345666; NID:9197295; P11N:AAA39004.1; P1D:4309469
 C/Superfamily: Immunoglobulin V region; immunoglobulin hamology
 F/36-114/Domains: immunoglobulin hamology <IMM>

Query Match 2.48; Score 7; DB 2; Length 128;
 Best Local Similarity 100.0%; Prod. No. 45;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 L1WILL 64
 |||||
 DB 7 L1WILL 13

RESULT 9
 KVM586
 Ia kappa chain precursor V regions (M63, AB22, PC9245, PC4950) - mouse
 C/Spectra: Mus musculus (house mouse)
 C/Dates: 02-Apr-1982 *sequence_revision 02-Apr-1982 *text_change 21-Jan-2000
 C/Accession: K00412; P01074; B01022; C94622; C92504; D91201; P11078; A01975
 R/Editor: V. J. Schachter, L.
 Biochemistry 17, 2392-2400, 1978
 A/Title: Primary structures of N terminal extra peptide segments linked to the variable
 expression of immunoglobulin genes.
 A/Reference number: A00412; M010-7825887
 A/Accession: M63
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-45

 A/Cross-references: DB:345666; NID:9197295; P11N:AAA39004.1; P1D:4309469
 Biochemistry 12, 760-771, 1973

A/Title: Mouse immunoglobulin chains. Pattern of sequence variation among kappa chain
 A/Reference number: A00774; M010-314025
 A/Accession: M63
 A/Contents: B60374
 A/Accession: B60374
 A/Molecule type: protein
 A/Residues: 21-45, 67-78, 53-75, 57-72, 79-86, 77-89, 141 <MK>
 A/Note: This sequence has since been revised in reference A00774
 R/Editor: D.J. Bell, M.J. Porter, M.
 Proc. Natl. Acad. Sci. U.S.A. 75, 4913-4917, 1978
 A/Title: Mechanisms of antibody diversity: multiple genes encode structurally related
 A/Reference number: A00774; M010-79012520
 A/Accession: M63; AB22
 A/Accession: B60822
 A/Molecule type: protein
 A/Residues: 1-54, 69-107 <M2>
 A/Accession: C94822
 A/Molecule type: protein
 A/Residues: 21-119, 77-121, 131-133 <M3>
 R/Editor: M.J. Gellerman, L. Loh, E.J. Schilling, J. Hood, L.
 Nature 276, 786-790, 1978
 A/Title: Rearrangement of genetic information may produce immunoglobulin diversity.
 A/Reference number: A00774; M010-7907152
 A/Accession: C93204
 A/Molecule type: protein
 A/Residues: 21-119, 77-121, 131-133 <M1>
 A/Accession: D93204
 A/Molecule type: protein
 A/Residues: 21-119, 77-121, 131-133 <M2>
 R/Editor: D.M. Jon, N.T. Hill, R.J. Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A/Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
 A/Reference number: P00771; M010-92381444
 A/Accession: P11078
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 21-122, 111
 A/Comment: The M63 precursor sequence is shown.
 C/Comment: An immunoglobulin heterotrimer subunit consists of two identical light (L)
 chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into
 C/Superfamily: immunoglobulin V region; immunoglobulin hamology
 C/Keywords: heterotrimer; immunoglobulin
 F/36-114/Domains: immunoglobulin hamology <IMM>
 F/36-114/Domains: immunoglobulin hamology <IMM>
 F/43-112/Domains: immunoglobulin hamology <IMM>

Query Match 2.48; Score 7; DB 1; Length 141;
 Best Local Similarity 100.0%; Prod. No. 45;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 L1WILL 64
 |||||
 DB 7 L1WILL 13

RESULT 10
 P11226
 Ia kappa chain precursor V region (M-1410) - mouse (treatment)
 C/Spectra: Mus musculus (house mouse)
 C/Dates: 17-Apr-1993 *sequence_revision 17-Apr-1993 *text_change 21-Jan-2000
 C/Accession: P11226
 R/Editor: W. J. Schachter, W. J. Schachter, M. J. Schachter, L. Loh, E. J. Schilling, J. Hood, L.
 Gene 121, 271-278, 1992
 A/Title: Combinatorial fusions of two chimeric antibodies directed to human CD4 and
 A/Reference number: P11224; M010-93077041
 A/Accession: P11226
 A/Molecule type: mRNA
 A/Residues: 1-131 <M1>
 A/Cross-references: DB:345666; NID:9197295; P11N:AAA39004.1; P1D:4309469
 A/Note: This mouse sequence was hybridized and fused with a human constant region gene

c2:Superfamily: immunoglobulin V region; immunoglobulin homology
 c3:Keywords: beta chain; kappa chain; immunoglobulin
 c4:Date: 28 Aug 1995 #sequence revision 19 Oct 1995 #text_change 21 Jan 2000
 c5:Accession: S55464
 c6:Comment: An immunoglobulin beta chain V region #status predicted - MA
 c7:Superfamily: immunoglobulin homology - IMM

Query Match 2.48E Score 7: 106.27 Length 143
 Best Local Similarity 100.00% Prod. No. 47
 Matches 7: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

57 58 LKWLIL 64
 111111
 ID 7 LKWLIL 13

RESULT 11

Query Match 2.48E Score 7: 106.27 Length 143
 Best Local Similarity 100.00% Prod. No. 47
 Matches 7: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

c1:Superfamily: immunoglobulin V region; mouse (fragment)
 c2:Species: Mus musculus (house mouse)
 c3:Date: 28 Aug 1995 #sequence revision 19 Oct 1995 #text_change 21 Jan 2000
 c5:Accession: S55464
 c6:Comment: A beta chain V region #status predicted - MA
 c7:Superfamily: immunoglobulin homology - IMM

A:Accession: S55464
 A:Reference: 1131 - EMBL
 A:Cross-reference: EMBL:U44044; NID:4476470; FID:AAA745471; PID:476720
 A:Superfamily: immunoglobulin V region; immunoglobulin homology
 c3:Keywords: immunoglobulin
 c4:Date: 28 Aug 1995 #sequence revision 19 Oct 1995 #text_change 21 Jan 2000

Query Match 2.48E Score 7: 106.27 Length 143
 Best Local Similarity 100.00% Prod. No. 47
 Matches 7: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

57 58 LKWLIL 64
 111111
 ID 7 LKWLIL 13

RESULT 12
 Query Match 2.48E Score 7: 106.27 Length 143
 Best Local Similarity 100.00% Prod. No. 47
 Matches 7: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

c1:Superfamily: immunoglobulin V region; mouse (tentative sequence)
 c2:Species: Mus musculus (house mouse)
 c3:Date: 28 Aug 1995 #sequence revision 19 Oct 1995 #text_change 21 Jan 2000
 c5:Accession: S55464
 c6:Comment: A beta chain V region #status predicted - MA
 c7:Superfamily: immunoglobulin homology - IMM

A:Accession: S55464
 A:Reference: 1131 - EMBL
 A:Cross-reference: EMBL:U44044; NID:4476470; FID:AAA745471; PID:476720
 A:Superfamily: immunoglobulin V region; immunoglobulin homology
 c3:Keywords: immunoglobulin
 c4:Date: 28 Aug 1995 #sequence revision 19 Oct 1995 #text_change 21 Jan 2000

A:Accession: S55464
 A:Reference: 1131 - EMBL
 A:Cross-reference: EMBL:U44044; NID:4476470; FID:AAA745471; PID:476720
 A:Superfamily: immunoglobulin V region; immunoglobulin homology
 c3:Keywords: immunoglobulin
 c4:Date: 28 Aug 1995 #sequence revision 19 Oct 1995 #text_change 21 Jan 2000

A:Reference number: A90474; MUIB:7440225

A:Accession: A90474

A:Molecule type: protein

A:Residues: 21-141 (M-2)

A:Note: The sequence is comparable with that of Mope 421 except in having 47 Gln, 51

c2:Comment: An immunoglobulin beta chain V region #status predicted - MA

c3:Superfamily: immunoglobulin V region; immunoglobulin homology

c4:Keywords: heterotrimer

c5:Date: 30 Sep 1994 #sequence revision 30 Sep 1994 #text_change 21 Jan 2000

c6:Accession: P0446

c7:Superfamily: immunoglobulin V region; immunoglobulin homology

c8:Keywords: heterotrimer

c9:Date: 30 Sep 1994 #sequence revision 30 Sep 1994 #text_change 21 Jan 2000

c10:Accession: P0446

c11:Superfamily: immunoglobulin V region; immunoglobulin homology

c12:Keywords: heterotrimer

c13:Date: 30 Sep 1994 #sequence revision 30 Sep 1994 #text_change 21 Jan 2000

c14:Accession: P0446

c15:Superfamily: immunoglobulin V region; immunoglobulin homology

c16:Keywords: heterotrimer

c17:Date: 30 Sep 1994 #sequence revision 30 Sep 1994 #text_change 21 Jan 2000

c18:Accession: P0446

c19:Superfamily: immunoglobulin V region; immunoglobulin homology

c20:Keywords: heterotrimer

c21:Date: 30 Sep 1994 #sequence revision 30 Sep 1994 #text_change 21 Jan 2000

c22:Accession: P0446

c23:Superfamily: immunoglobulin V region; immunoglobulin homology

c24:Keywords: heterotrimer

c25:Date: 30 Sep 1994 #sequence revision 30 Sep 1994 #text_change 21 Jan 2000

c26:Accession: P0446

c27:Superfamily: immunoglobulin V region; immunoglobulin homology

c28:Keywords: heterotrimer

c29:Date: 30 Sep 1994 #sequence revision 30 Sep 1994 #text_change 21 Jan 2000

c30:Accession: P0446

c31:Superfamily: immunoglobulin V region; immunoglobulin homology

c32:Keywords: heterotrimer

c33:Date: 30 Sep 1994 #sequence revision 30 Sep 1994 #text_change 21 Jan 2000

c34:Accession: P0446

Query Match 2.38; Score 7; DB 2; Length 140;
 Best Local Similarity 100.00; Pred. No. 37;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 58 ELWVLL 64
 |||||
 IQ 7 ELWVLL 13

RESULT 15

12114
 Hypothetical protein JCR.8 - Caenorhabditis elegans
 c-Spectra: Caenorhabditis elegans
 c-Dat: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
 c-Accession: 12114
 c-Addition: J.
 Submitted to the EMBL Data Library: November 1996
 A-Reference number: Z19699
 A-Accession: 12114
 A-Status: preliminary; translated from cDNA/EMBL/DDNJ
 A-Molecule type: DNA
 A-Residues: 1159 aa
 A-Cross references: EMBL:Z92274; PDB:CAH5225.1; GENB:GN00022; CDS:JCR.8
 A-Experimental source: clone JCR
 c-Notes:
 A-Name: CDS:JCR.8
 A-Map position: 4
 A-Introns: 8/27 4+/4
 c-Superfamily: Caenorhabditis hypothetical protein CA0H1.5

Query Match 2.38; Score 7; DB 2; Length 159;
 Best Local Similarity 100.00; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 244 ELIDAI 240
 |||||
 IQ 26 ELIDAI 32

Search completed: August 12, 2002, 14:01:29
 Job time: 216 sec

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[illegible][illegible]

27	352	ECRTEPSP	409	
28	111	111	111	
1	251	ECRTEPSP	408	
RESULT	6			
Q9NYW3				
10	Q9NYW3	PRELIMINARY;	PR1:	318 AA.
AC	Q9NYW3			
DI	01-JUN-2000 (17EMBLrel, 15, created)			
FE	01-JUN-2000 (17EMBLrel, 15, last sequence update)			
DI	01-JUN-2001 (17EMBLrel, 17, last annotation update)			
DE	CANDIDATE TASTE RECEPTOR T2R7.			
OS	Homo sapiens (Human).			
OC	Tetrapoda; Mammalia; Chordata; Mammalia; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX	Mbl_caxid:9606;			
RN	111			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE:20222571; PubMed 10761944;			
KA	Adler E., Hoon M.A., Mueller K.L., Chandrasekhar J., Ryba N.J.P., Zuker C.S.;			
R7	"A novel family of mammalian taste receptors.";			
KL	Cell 100:693-702(2000).			
DR	EMBL: AF227133; AAF3904.1;			
DR	InfoProc: IPR000276; GPCR_Rhodopsin.			
DR	PROSITE: PS02662; G_PROTEIN_RECEP_F1_2: 1.			
SW	Receptor			
SEQUENCE	418 AA: 36549 MW: 4187208248.274800 CIRC64;			

Query Match	Score	544:	DB4:	Length	316:
Post Local Similarity	40.0%				
Matches	122:	Conserved	58:	Mismatches	109:
				Indels	16:
				Gaps	
07	12	1	1	1	1
08	12	1	1	1	1
09	12	1	1	1	1
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11	12	1	1	1	1
12	12	1	1	1	1
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14	12	1	1	1	1
15	12	1	1	1	1
16	12	1	1	1	1
17	12	1	1	1	1
18	12	1	1	1	1
19	12	1	1	1	1
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33	12	1	1	1	1
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35	12	1	1	1	1
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89	12	1	1	1	1
90	12	1	1	1	1
91	12	1	1	1	1
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93	12	1	1	1	1
94	12	1	1	1	1

geometry: Mat. Th. (40:98); Sequences 404; 108 11; Length 207;
 host: Journal: Statistics 40; 50; Prod. No. 1, 40 40;
 Mathematics: 141; Abstracts: 108; Index: 16; OAPS: 7;

245 ELYSIUM SYMBIOTICALLY INHIBITS BACTERIAL GROWTH 297

RESULT 10

[illegible]

```

Query Match      28.28; Score 451; DB 11; Length 245;
Best Local Similarity 40.68; Pred. No. 4,2e-30;
Matches 94; Conservative 54; Mismatches 81; Indels 10; Gaps 4;

QY 1 7 PEGYTFEASQITLTAASVETLWLLINWSTVLNPAENGVETT ANIMAVINHEFS 95
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 6 KKRKSNVIGSLTAIALSRIALMLLVSWMLVYQGMVTKRKVSIMSTWITFNQSS 65

QY 46 NMIAITTSIFYLRIANFSNFIHLKREKVSILVMLLGPLFLACHLFTIMNEIVPT 155
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 66 LWFANSTSEVEYFANRSPFTYFVFPKYVMISCTIMSTHFGYNIIMATFNILL 125

QY 156 FEEDGNMFWLEESAM FEEDVYVMAALLVFIILLSSMELHPSLGMALPMO 210
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 126 TTYVSMSTSLNRTQSLNIFRAN--TMF GTFVAVSLVFLVLSLNRHQRMO 181

QY 211 LHKNSQIPSTKWHKALQIVISPLALCAIYPLSIMSVSPGSLNKPVEPKAKIRPS 270
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 182 HSAHSCPFASIKAHFAIGTILASLLVSTFPLSHVAKWSALLPEFTILLITGVAPTA 241

QY 271 YPSI 274
      | | |
DB 242 FPSV 245

```

Search completed: August 12, 2002, 13:57:47
 Job time: 458 sec

[illegible]

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

C	1	940	100.0	212739	2	AC0186430	AC0186430	Homo sapiens
C	2	823.4	89.6	314703	2	AC0187434	AC0187434	Homo sapiens
C	3	822.8	88.5	162486	2	AC018851	AC018851	Homo sapiens
C	4	822.8	88.5	314700	2	AC0187434	AC0187434	Homo sapiens
C	5	797.4	85.7	335234	2	AC0796255	AC0796255	Homo sapiens
C	6	796.4	85.6	162480	2	AC018851	AC018851	Homo sapiens
C	7	773.2	83.1	90	6	AC0977751	AC0977751	Homo sapiens
C	8	751.6	80.8	960	6	AC0977746	AC0977746	Homo sapiens
C	9	751.4	80.8	900	6	AC0977746	AC0977746	Homo sapiens
C	10	741.2	74.7	930	6	AC0977755	AC0977755	Homo sapiens
C	11	745.8	79.1	930	6	AC0977757	AC0977757	Homo sapiens
C	12	691.4	71.3	173735	9	AC0065518	AC0065518	Homo sapiens
C	13	684.4	73.6	903	6	AC0977743	AC0977743	Homo sapiens
C	14	620.2	65.9	682	6	AC0299347	AC0299347	Homo sapiens
C	15	407.8	43.8	1394	6	AC0978348	AC0978348	Homo sapiens
C	16	372.8	40.1	268913	2	AC106253	AC106253	Homo sapiens
C	17	372.4	40.0	174554	2	AC103303	AC103303	Homo sapiens
C	18	340.8	36.6	954	6	AC0977721	AC0977721	Homo sapiens
C	19	340.8	36.6	954	6	AC1275168	AC1275168	Homo sapiens
C	20	340.8	36.6	190002	2	AC0986649	AC0986649	Homo sapiens
C	21	322.6	34.7	173534	2	AC0989886	AC0989886	Homo sapiens
C	22	308.2	33.1	912	6	AC0977719	AC0977719	Homo sapiens
C	23	308.2	33.1	912	6	AC1273137	AC1273137	Homo sapiens
C	24	298	32.0	1482	6	AC0978238	AC0978238	Homo sapiens
C	25	293.6	31.6	397	6	AC0977732	AC0977732	Homo sapiens
C	26	287.4	30.9	1465	6	AC0978446	AC0978446	Homo sapiens
C	27	281.4	30.5	165	6	AC0977732	AC0977732	Homo sapiens
C	28	281.8	30.3	1103	6	AC0978446	AC0978446	Homo sapiens
C	29	281	30.2	268913	2	AC106253	AC106253	Homo sapiens
C	30	280.6	30.2	1316	6	AC0978430	AC0978430	Homo sapiens
C	31	279.8	30.1	1354	6	AC0978432	AC0978432	Homo sapiens
C	32	271.4	28.6	17559	6	AC097802	AC097802	Homo sapiens
C	33	266.2	28.6	175594	2	AC103303	AC103303	Homo sapiens
C	34	263.4	28.3	173534	2	AC0989886	AC0989886	Homo sapiens
C	35	263	28.0	2637	6	AC0978432	AC0978432	Homo sapiens
C	36	254	27.3	1339	6	AC0978416	AC0978416	Homo sapiens
C	37	252.8	27.2	945	10	AC1273135	AC1273135	Homo sapiens
C	38	252.8	27.2	1886	6	AC097786	AC097786	Homo sapiens
C	39	252.2	27.1	339	9	AC1264628	AC1264628	Homo sapiens
C	40	252.2	27.1	1371	6	AC0979300	AC0979300	Homo sapiens
C	41	251.8	27.1	4394	6	AC0977844	AC0977844	Homo sapiens
C	42	249.8	26.9	1399	6	AC0978244	AC0978244	Homo sapiens
C	43	247.6	26.6	518	10	AC1273144	AC1273144	Homo sapiens
C	44	243.2	26.2	1432	6	AC097844	AC097844	Homo sapiens
C	45	243	26.0	945	6	AC097728	AC097728	Homo sapiens

REFERENCES

RESULT	1
AC018630	21,2789 bp, 1NA, 11001, 11011, 14, 667, 2001
LOCUS	HOMO SAPIENS CHROMOSOME 12, STRAIN HET 673015, WGBRINT PRAT
DEFINITION	SEQUENCE, 2 unordered pieces.
ACCESSION	AC018630
VERSION	AC018630.44 GI:16041429
KEYWORDS	HTG; HUS; PHASE1; HUS; PRAT1; HUS; FULL10P; HUS; ACT10P11N.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryotes: Metazoa; Chordata; Stamata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
	1 (bases 1 to 212789)
	Buzny, A. M., Adams, C. J., Adio, O. S., Buzny, A. M., Adams, C. J., Allen, C. J.

[illegible]

[illegible][illegible][illegible]

[illegible]

Query Match	85.50%	Score 796.47	Id 27	Length 162380
Host Local Similarity	94.70%	Prod. No. 4.80	197	
Matches after conservative	0	Mismatches	76	Indels 1
				Gaps 1

[illegible][illegible]

RESULT	7
AX097751	
TACUS	980 bp DNA
DEFINITION	Sequence 57 from Patient W0118050.
ACCESSION	AX097751
VERSION	AX097751.1 GI:13514894
KEYWORDS	.
SOURCE	Human;
ORGANISM	Homo sapiens
REFERENCE	EKKAYOTI; MEEZUM; OTHODATA; CHAIKHA; VORICHAK; EIT-CHONGMUT; Nematode Pathogen Primases; Paratuberculosis; Biondiac; Homo. 1 (bases 1 to 980)
AUTHORS	ZIEKE, S., ADLER, J. F., PETER, N., MCLELLAN, K. and BOON, M.
TITLE	12F Taste Receptor Family
JOURNAL	Patient W0118050 A 57 15 MAR 2001 THE RESEARCH OF THE UNIVERSITY OF CALIFORNIA (US) THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US) LOCATION/Qualities 1. 1980
FEATURES	
SOURCE	

[illegible]

Query Match:	83.1%	Score:	733.27	len:	106.07	length:	9402
Host Local Similarity:	89.5%	Pred. No.:	10-1611				
Matches:	932	Count out:	99	Indels:	0	caps:	0

6) `addTactant[acTactantIndex] = addTactant[acTactantIndex + 1]`

[illegible][illegible][illegible]

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1998	401	4.01
1999	401	4.01
2000	401	4.01
2001	401	4.01
2002	401	4.01
2003	401	4.01
2004	401	4.01
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2018	401	4.01
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2094	401	4.01
2095	401	4.01
2096	401	4.01
2097	401	4.01
2098	401	4.01
2099	401	4.01
2100	401	4.01

[illegible]

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CY	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821


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07 64 ttttaattgaacttcatacgaatgaattccattgaatgattcaagaaagaaatc 123
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08 647 tcttctaaatcttcttcttcttcttcttcttcttcttcttcttcttcttctt 596
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09 124 tcttctaaatcttcttcttcttcttcttcttcttcttcttcttcttcttctt 183
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10 597 tcttctaaatcttcttcttcttcttcttcttcttcttcttcttcttcttctt 656
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07 184 ttttttgaactgaattcgaactgaattgaactgaactgaactgaactgaact 243
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07 244 acttactgaactgaactgaactgaactgaactgaactgaactgaactgaactga 303
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10 1197 tttttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 1247
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
07 784 atggttgaactgaactgaactgaactgaactgaactgaactgaactgaactga 843
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
10 1248 ctgtttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 1307
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
07 844 aaaaagaaatcttgaactgaactgaactgaactgaactgaactgaactgaact 903
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
10 1308 gaaaagaaatcttgaactgaactgaactgaactgaactgaactgaactgaact 1367
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
07 904 aaaaagaaatcttgaactgaactgaactgaactgaactgaactgaactgaact 930
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
10 1308 aaaaagaaatcttgaactgaactgaactgaactgaactgaactgaactgaact 1394
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Search completed: August 12, 2002, 12:50:58
Job Time: 655.3 sec



RP SEQUENCE FROM N.A.
 RX MEDLINE 2022571; PubMed 1076194;
 RA Adler E., Heon M.A., Mueller K.L., Chandrasekar J., Kyba N.J.P.,
 Zaker C.S.;
 RT "A novel family of mammalian taste receptors."
 RL Cell 100:593-702(2000).
 DR EMBL AF227157; A0431910.1; -;
 KW Receptor.
 SQ SEQUENCE 403 AA; 65118 MW; 7560P56E2F66B95 CRR94;

Query Match 2.98; Score 11; DB 4; Length 412;
 Best Local Similarity 100.0%; Prod. No. 0.0042;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 SEPTILKIA 111
 DB 104 SEPTILKIA 112

RESULT 4
 QJRKER PRELIMINARY PRG 405 AA.
 AC QJRKER
 DT 01-oct-2000 (1:EMBLrel. 15; Created)
 DT 01-oct-2000 (1:EMBLrel. 15; Last sequence update)
 DT 01-oct-2000 (1:EMBLrel. 15; Last annotation update)
 DE CANAL TASTE RECEPTOR RT2R2.
 DE RATTUS NORVEGICUS (Rat).
 DE ENKRYPTOL: Metazoa; Chordata; Vertebrata; Euteleostomi;
 DE Mammalia; Eutheria; Rodentia; Sciurodonta; Muridae; Murinae; Rattus;
 DE NCBI_TaxID 10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 2022571; PubMed 1076194;
 RA Adler E., Heon M.A., Mueller K.L., Chandrasekar J., Kyba N.J.P.,
 Zaker C.S.;
 RT "A novel family of mammalian taste receptors."
 RL Cell 100:593-702(2000).
 DR EMBL AF227157; A0431910.1; -;
 KW Receptor.
 SQ SEQUENCE 403 AA; 65118 MW; 7560P56E2F66B95 CRR94;

Query Match 2.98; Score 10; DB 11; Length 403;
 Best Local Similarity 100.0%; Prod. No. 0.007;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 SEPTILKIA 111
 DB 104 SEPTILKIA 112

RESULT 1
 QJRKER PRELIMINARY PRG 403 AA.
 AC QJRKER
 DT 01-oct-2000 (1:EMBLrel. 15; Created)
 DT 01-oct-2000 (1:EMBLrel. 15; Last sequence update)
 DT 01-oct-2000 (1:EMBLrel. 15; Last annotation update)
 DE CANAL TASTE RECEPTOR RT2R1.
 DE RATTUS NORVEGICUS (Rat).
 DE ENKRYPTOL: Metazoa; Chordata; Vertebrata; Euteleostomi;
 DE Mammalia; Eutheria; Rodentia; Sciurodonta; Muridae; Murinae; Rattus;
 DE NCBI_TaxID 10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 2022571; PubMed 1076194;
 RA Adler E., Heon M.A., Mueller K.L., Chandrasekar J., Kyba N.J.P.,
 Zaker C.S.;
 RT "A novel family of mammalian taste receptors."
 RL Cell 100:593-702(2000).
 DR EMBL AF240767; A043505.1; -;

RP SEQUENCE FROM N.A.
 RX MEDLINE 2022571; PubMed 1076194;
 RA Adler E., Heon M.A., Mueller K.L., Chandrasekar J., Kyba N.J.P.,
 Zaker C.S.;
 RT "A novel family of mammalian taste receptors."
 RL Cell 100:593-702(2000).
 DR EMBL AF227157; A0431910.1; -;
 KW Receptor.
 SQ SEQUENCE 403 AA; 65118 MW; 7560P56E2F66B95 CRR94;

Query Match 2.98; Score 9; DB 4; Length 403;
 Best Local Similarity 100.0%; Prod. No. 0.94;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 SEPTILKIA 111
 DB 104 SEPTILKIA 112

RESULT 5
 QJRKER PRELIMINARY PRG 444 AA.
 AC QJRKER
 DT 01-oct-2000 (1:EMBLrel. 15; Created)
 DT 01-oct-2000 (1:EMBLrel. 15; Last sequence update)
 DT 01-oct-2000 (1:EMBLrel. 15; Last annotation update)
 DE TASTE RECEPTOR RT2R2.
 DE RATTUS NORVEGICUS (Rat).
 DE ENKRYPTOL: Metazoa; Chordata; Vertebrata; Euteleostomi;
 DE Mammalia; Eutheria; Rodentia; Sciurodonta; Muridae; Murinae; Rattus;
 DE NCBI_TaxID 10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 2022571; PubMed 1076194;
 RA Adler E., Heon M.A., Mueller K.L., Chandrasekar J., Kyba N.J.P.,
 Zaker C.S.;
 RT "A novel family of mammalian taste receptors."
 RL Cell 100:593-702(2000).
 DR EMBL AF240767; A043505.1; -;
 KW Receptor.
 SQ SEQUENCE 444 AA; 68163 MW; A160B2470E610E CRR94;

Query Match 2.98; Score 9; DB 11; Length 444;
 Best Local Similarity 100.0%; Prod. No. 1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 ANQILKIA 52
 DB 49 ANQILKIA 57

RESULT 6
 QJRKER PRELIMINARY PRG 141 AA.
 AC QJRKER
 DT 01-oct-2000 (1:EMBLrel. 15; Created)
 DT 01-oct-2000 (1:EMBLrel. 15; Last sequence update)
 DT 01-oct-2000 (1:EMBLrel. 15; Last annotation update)
 DE TASTE RECEPTOR RT2R10 (FRAGMENT).
 DE RATTUS NORVEGICUS (Rat).
 DE ENKRYPTOL: Metazoa; Chordata; Vertebrata; Euteleostomi;
 DE Mammalia; Eutheria; Rodentia; Sciurodonta; Muridae; Murinae; Rattus;
 DE NCBI_TaxID 10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 2022571; PubMed 1076194;
 RA Adler E., Heon M.A., Mueller K.L., Chandrasekar J., Kyba N.J.P.,
 Zaker C.S.;
 RT "A novel family of mammalian taste receptors."
 RL Cell 100:593-702(2000).
 DR EMBL AF240767; A043505.1; -;

KM Receptor.
 E1 N_LINKER 141 131
 S0 SEQUENCE 141 AA: 15358 MW: 175A194D0FAD0F54 CR664;

Query Match
 Post Local Similarity 100.0% Prod. No. 5;
 Matches 8: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

QY 24 NFE1A1N 41
 1111111
 DB 29 NFE1A1N 46

RESULT 7
 064215 PRELIMINARY: PRT: 159 AA.

AC 064215;
 DI 01-AUG-1998 (ITEMBL01.07, Created)
 DI 01-AUG-1998 (ITEMBL01.07, Last sequence update)
 DI 01-DEC-2001 (ITEMBL01.19, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE 1 (EC 1.9.3.1) (FRAGMENT).
 GN Cyt.
 OS Peripatoides novaezealandiae.
 OX Mitochondrion.
 OC Eukaryota; Metazoa; Chordophora; Peripatoidae; Peripatoides.
 OX NCBL TaxID 49105;
 RN [1]

RE SEQUENCE FROM N.A.
 RC STRAIN TOWA WALK NEW ZEALAND;
 RX MEDLINE=99047288; PubMed=9878244;
 RA Gleeson D.M., Rowell D.M., Tait N.N., Hirston P.A., Higgins A.V.;
 RT "Physiological relationships among cytochrome c oxidase subunit 1 gene."
 RL Mol. Phylogenet. Evol. 10:237-248(1998).
 GN FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 4 FORM THE FUNCTIONAL COMPLEX OF THE ENZYME. COMPLEX 1 IS THE
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 GN AND COPPER B (BY SIMILARITY).
 GN CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 FERROCYTOCHROME C;
 GN COFACTOR: HEMES A, A3, AND COPPER B (BY SIMILARITY).
 GN PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 GN SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 INNER MEMBRANE (BY SIMILARITY).
 GN SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DE EMBL: D062420; AA096419.1;
 DE F000700; F0000883; C001.
 DE Pfam: PF00115; C001.1.
 KW Cytochrome. Heme. Inner membrane. Mitochondrion. Oxidoreductase.
 KW Respiratory chain. Transmembrane.
 FT N-TER 1
 FT N-TER 1
 FT N-TER 159
 S0 SEQUENCE 159 AA: 17369 MW: 4540812F66F25CA CR664;

Query Match
 Post Local Similarity 100.0% Prod. No. 5;
 Matches 8: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

QY 104 SEMILLIS 201
 1111111
 DB 24 SEMILLIS 31

RESULT 8
 09NM24 PRELIMINARY: PRT: 176 AA.
 DI 01-DEC-2001 (ITEMBL01.15, Created)

DI 01-OCT-2000 (ITEMBL01.15, Last sequence update)
 DI 01-OCT-2000 (ITEMBL01.15, Last annotation update)
 DE GINA FL120519 FIS, GIGNE KAT10365.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eulioria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBL TaxID 9606;
 RN [1]

RE SEQUENCE FROM N.A.
 RA Watanabe K., Kamegaki A., Takura S., Yamaoka M., Tashiro H., and T.
 RA Suzuki Y., Ohayashi M., Nishi T., Shibahara T., Tanaka T.,
 RA Nakamura Y., Isono T., Sugano S.;
 RT "NEO human cDNA sequencing project."
 RL Submitted (FEB-2000) to the FMB/GenBank/EMBL databases.
 DE EMBL: AK000526; U069124.1;
 S0 SEQUENCE 176 AA: 18584 MW: 101667070697067 CR664;

Query Match
 Post Local Similarity 100.0% Prod. No. 6.4;
 Matches 8: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

QY 58 LLWILLIN 65
 1111111
 DB 8 LLWILLIN 15

RESULT 9
 09JKA2 PRELIMINARY: PRT: 238 AA.

AC 09JKA2;
 DI 01-OCT-2000 (ITEMBL01.15, Created)
 DI 01-OCT-2000 (ITEMBL01.15, Last sequence update)
 DI 01-DEC-2001 (ITEMBL01.19, Last annotation update)
 DE CARBOXYATE TASTE RECEPTOR T2R2 (TAS2R2).
 GN TAS2R2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eulioria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBL TaxID 10090;
 RN [1]

RE SEQUENCE FROM N.A.
 RC STRAIN DRA/20;
 RX MEDLINE=20247397; PubMed 10766423;
 RA Marstrand H., Møllerlyng J., F., Buck L.H.;
 RT "A family of candidate taste receptors in human and mouse."
 RL Nature 404:601-604(2000).
 DE EMBL: AF247742; AA06409.1;
 DE M0011800257; TAS2R10.
 KW Receptor.
 FT N-TER 1
 FT N-TER 1
 FT N-TER 238
 S0 SEQUENCE 238 AA: 27112 MW: 9096707660947 CR664;

Query Match
 Post Local Similarity 100.0% Prod. No. 8.3;
 Matches 8: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

QY 108 LXINFSN 115
 1111111
 DB 74 LXINFSN 81

RESULT 10
 09JKA2 PRELIMINARY: PRT: 243 AA.
 AC 09JKA2;
 DI 01-OCT-2000 (ITEMBL01.15, Created)
 DI 01-OCT-2000 (ITEMBL01.15, Last sequence update)
 DI 01-DEC-2001 (ITEMBL01.19, Last annotation update)
 DE CANDIDATE TASTE RECEPTOR TR43 (TAS2R43).
 GN TAS2R43.

OS Mus musculus (Mouse);
 AC Eukaryotic Metazoa: Chordata: Vertebrata: Euteleostomi;
 AC Mammalia: Eutheria: Rodentia: Sciurostomatia: Muridae: Murinae: Mus;
 CX NCBI_TaxID:10090;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE:20227409; PubMed:10766242;
 KA Motomura H., Motomura A. P., Inoue T. P.,
 KA "A family of vertebrate taste receptors in human and mouse."
 KA Nucleic Acids Res 30(4):2000;
 LR EMBL: AF247344; AAF43430.1;
 LR MIM: 601194; L882133;
 KW Receptor;
 RT NON-TEP
 RT NON-TEP
 SO SOURCE: 245 AA; 20110 MW; DAA014AFV45E002.076943;

Query Match 2.6M; Score 8; DB 11; Length 245;
 Best Local Similarity: 100.0%; Prod. No. 84;
 Matches: 8; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 LKIANFSN 115
 DB 1111111
 DB 1 LKIANFSN 62

RESULT 11

ID Q9JKT9 PRELIMINARY: PRT: 245 AA.

AC Q9JKT9: (EMBL:01, 15, (Created))

DT 01-OCT-2000 (EMBL:01, 15, Last sequence update)

DI 01-OCT-2000 (EMBL:01, 15, Last annotation update)

DE CANDIDATE TASTE RECEPTOR 12K10 (Eukaryotic)

OS Mus musculus (Mouse);
 AC Eukaryotic Metazoa: Chordata: Vertebrata: Euteleostomi;
 AC Mammalia: Eutheria: Rodentia: Sciurostomatia: Muridae: Murinae: Mus;
 CX NCBI_TaxID:10090;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE:20227409; PubMed:10766242;
 KA Motomura H., Motomura A. P., Inoue T. P.,
 KA "A family of vertebrate taste receptors in human and mouse."
 KA Nucleic Acids Res 30(4):2000;
 LR EMBL: AF247344; AAF43430.1;
 LR MIM: 601194; L882133;
 KW Receptor;
 RT NON-TEP
 RT NON-TEP
 SO SOURCE: 245 AA; 20650 MW; Q9JKT9E2770085.076943;

Query Match 2.6M; Score 8; DB 11; Length 245;
 Best Local Similarity: 100.0%; Prod. No. 84;
 Matches: 8; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 4 LKIANFSN 115
 DB 1111111
 DB 4 LKIANFSN 115

RESULT 12

ID Q9JKT9 PRELIMINARY: PRT: 438 AA.

AC Q9JKT9: (EMBL:01, 15, (Created))

DT 01-OCT-2000 (EMBL:01, 15, Last sequence update)

DI 01-OCT-2000 (EMBL:01, 15, Last annotation update)

DE CANDIDATE TASTE RECEPTOR 12K10 (Eukaryotic)

CN BBH20.140;

OS Neurospora crassa;

AC Eukaryotic Fungi: Ascomycota: Pezizomycotina: Sordariomycetes;

AC Sordariaceae: Sordariaceae: Neurospora;

CX NCBI_TaxID:5141;
 RN 11
 RP SEQUENCE FROM N.A.
 KA Schiller G., Anu V., Holsen J., Brandt P., Fairman H., Holland R.,
 KA Mykura G., Myers H.W., Munnhaupt G.,
 KA Submitted (May 2000) to the EMBL/GenBank/DBJ databases;
 RN 12
 RP SEQUENCE FROM N.A.
 KA German Neurospora genome project;
 RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases;
 LR EMBL: AF559443; DAB01461.2;
 SO SOURCE: 406 AA; 42875 MW; 2770PB61E7FAF452.076943;

Query Match 2.6M; Score 8; DB 3; Length 406;
 Best Local Similarity: 100.0%; Prod. No. 10;
 Matches: 8; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 121 LKREKSV 126
 DB 1111111
 DB 241 LKREKSV 246

RESULT 13

ID Q9JKT9 PRELIMINARY: PRT: 407 AA.

AC Q9JKT9: (EMBL:01, 15, (Created))

DT 01-OCT-2000 (EMBL:01, 15, Last sequence update)

DI 01-OCT-2000 (EMBL:01, 15, Last annotation update)

DE CANDIDATE TASTE RECEPTOR 12K10 (Eukaryotic)

OS Homo sapiens (Human);
 AC Eukaryotic Metazoa: Chordata: Vertebrata: Euteleostomi;
 AC Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo;
 CX NCBI_TaxID:9606;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE:20227409; PubMed:10766242;
 KA Adler B., Hoon M.A., Mueller K.L., Chandrasekhar J., Ryba N.J.P.,
 KA Zuker C.S.;
 KA "A novel family of mammalian taste receptors."
 KA Cell 100:693-702(2000);
 LR EMBL: AF227186; AAF43909.1;
 KW Receptor;
 SO SOURCE: 407 AA; 45465 MW; Q9JKT9D65A6E7106.076943;

Query Match 2.6M; Score 8; DB 4; Length 407;
 Best Local Similarity: 100.0%; Prod. No. 10;
 Matches: 8; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 108 LKIANFSN 115
 DB 1111111
 DB 108 LKIANFSN 115

RESULT 14

ID Q9JKT9 PRELIMINARY: PRT: 408 AA.

AC Q9JKT9: (EMBL:01, 15, (Created))

DT 01-OCT-2000 (EMBL:01, 15, Last sequence update)

DI 01-OCT-2000 (EMBL:01, 15, Last annotation update)

DE CANDIDATE TASTE RECEPTOR 12K10 (Eukaryotic)

OS Eukaryotic Metazoa: Chordata: Vertebrata: Euteleostomi;
 AC Mammalia: Eutheria: Rodentia: Sciurostomatia: Muridae: Murinae: Rattus;
 CX NCBI_TaxID:10156;
 RN 11

RP SEQUENCE FROM N.A.
 KX MEDLINE 2022571; PubMed-10761944;
 RA Adler E., Boon M.A., Mueller K.L., Chandrasekar J., Ryba N.J.P.,
 RA Zuker C.S.;
 RI "A novel family of mammalian taste receptors";
 RL JOL 100:693-702(2000);
 DR EMBL AF227142; AAF43915.1;
 KW RECEPTOR;
 SQ SEQUENCE 408 AA; 65052 MW; 00804193204E043 CIRC64;

Query Match: 2.68; Score 8; DB 11; Length 408;
 Post Local Similarity 100.0%; Prod. No. 10;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 LKIANFSN 115
 108 LKIANFSN 115

RESULT 15

Q9CJ93 PRELIMINARY; PRT; 411 AA.
 AC Q9CJ93;
 DE 01-JUN-2001 (FEBBLR1.17, created)
 DT 01-JUN-2001 (FEBBLR1.17, last sequence update)
 DI 01-OCT-2001 (FEBBLR1.18, last annotation update)
 DE GLYCOSYL TRANSFERASE.
 GN YHA1.
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 OC Lactococcus;
 OX NCBI_TaxID=1460;
 RN 111
 RP SEQUENCE FROM N.A.
 RC STRAIN 121403;
 RX MEDLINE 2128186; PubMed-11337471;
 RA Bolotin A., Wincker P., Manger S., Jallou O., Malarme K.,
 RA Weissenbach J., Ehrlich S.D., Sorokin A.;
 RI "The complete genome sequence of the lactic acid bacterium Lactococcus
 RI lactis ssp. lactis 121403";
 RL Genome Res. 11:741-754(2001);
 LR EMBL AF006249; AAK04055.1;
 DR InterPro: IPRO01174; Glycos_Transf_2;
 DR Pfam: PF00545; Glycos_Transf_2; 1;
 KW Transferase; Complete Proteome;
 SQ SEQUENCE 411 AA; 35372 MW; F60809C95C8E4527 CIRC64;

Query Match: 2.68; Score 8; DB 16; Length 411;
 Post Local Similarity 100.0%; Prod. No. 10;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 LSTFYLIK 169
 102 LSTFYLIK 169

Search completed: August 12, 2002, 14:00:49
 Job time: 266 sec


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1% EMBL: A6100206: A672104.1: -
1% InterPro: IPR000276: cpr_kbafspn
1% Pfam: PF00001: 7tm1: 1

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BA O'Dowd J.F., Helbert M., Chan A., Hogg H.B., Tsui L.C., Kennedy J.L., Shi X., Porteous A., George S.B., Maynard J., RI "A human gene that shows identity with the gene encoding the

[illegible]

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COX NCBI_TaxID-9825;

FT	TRANSMEH	285	308		7 (POTENTIAL)
ET	DOMAIN	309	360		CYTOPLASMIC (POTENTIAL).
ET	DOMAIN	343	346		POLY-SER.
ET	CARD-ORFD	2	2		R-T (IN REF. 2)) (POTENTIAL).
ET	CARD-ORFD	183	183		N-T (IN REF. 2)) (POTENTIAL).
ET	CARD-ORFD	194	194		N-T (IN REF. 2)) (POTENTIAL).
ET	DLSLEFLD	110	187		BY SIMILARITY.
ET	CONELICT	4	4		T - T (IN REF. 2) .
ET	CONELICT	145	145		S - S (IN REF. 2) .
ET	CONELICT	181	181		E - E (IN REF. 2) .
ET	CONELICT	205	205		H - D (IN REF. 2) .
ET	CONELICT	221	221		K - F (IN REF. 2) .
ET	CONELICT	241	241		V - L (IN REF. 2) .
ET	CONELICT	246	246		G - A (IN REF. 2) .
ET	CONELICT	293	293		G - A (IN REF. 2) .
ET	CONELICT	311	311		F - S (IN REF. 2) .
SD	SEQUENCE	460 AA	41462 MW	970860462509AA	PROT. ID.
<hr/>					
Query Match:		7.481	Score 1171	DB 1:	Length 4601
Post Local Similarity		7.481	Freq. No. 0.175		
Matches	51:	Conservative	44:	Mismatches	75:
<hr/>					
QY	4 HPIPLESVVVFVTCNPFAPFVAIVNSIPWFVGKPTSPADQIIIAVNS-----	54			
DB	111 111 111 111 111 111 111 111 111 111 111 111 111 111 111				
DB	41 FLPLPS-----LVELLDLPNSVVLEV-LFEVEFLK-SMTVEVLNLALSLLEWLSLP	94			
QY	55 -----RVCGL-----WLLIMYSVTLANTRGVEERTVANIMAVNIHSNNM	98			
DB	111 111 111 111 111 111 111 111 111 111 111 111 111 111 111				
DB	94 PWTATACQVPEVRLACKLVSNQQLVAVSYSGTFHMLMSLT-----RLAIVAVAFSLK	147			
QY	99 ATTIISTPYLLIANFSNEIFELKKRKRSVTHVMIGIQLLANCLVAMNLRKEE	158			
DB	111 111 111 111 111 111 111 111 111 111 111 111 111 111 111				
DB	148 ARILLVGVLIISLIMSVAFAASLP-----DLSESTC-VLENHHYCKIQVS	192			
QY	159 FKNWKGKTFKSAFYSSNMVIVGMNVVGFIIITISPMELCSL--CHIEKER	209			
DB	111 111 111 111 111 111 111 111 111 111 111 111 111 111 111				
DB	193 VNSTLVLE-----LSSEFVNGVCTIIVGIMLFWSMILPTIGHFEEFF	277			
<hr/>					
RESULT 11					
CD2_HUMAN					
ID	CD2_HUMAN	STANDARD:	PRTS:	346 AA.	
AV	QVNS752-QVNFV27:				
D1	01 MAR 2002 (Ref. 4): Created)				
D1	01 MAR 2002 (Ref. 4): Last sequence update)				
D1	01 MAR 2002 (Ref. 4): Last annotation update)				
DE	Cystic-fibrosis type III receptor 2 (CYSLTR2) (PSC0104). (M937) (HPR321).				
GN	CYSLTR2 OR CYSLT2 OR CYSLTZR.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Primates; Catarrhini; Hominoidea; Homo.				
OX	NCBI TaxID=6066;				
NN	SEQUENCE FROM N.A.				
RP	GENBANK F049142				
RX	MEDLINE 20459128; PubMed 10851292;				
RA	Bryant C.E., Chowdhury I., Fletcher R., Mayes T.,				
RA	Boyd S., Stevens R., Hollenhorst J.N., Abramowitz M., Cheng R.,				
RA	Williams J.L., Li Zong Z., Lin Q., Ma L., Clements M.K., Lombardo N.,				
RA	Lin Y., Austin J.P., George S.R., O'Neill G.P., Matthews R.M.,				
RA	Lynch K.E., Evans D.F.				
RT	"Characterization of the human cystic-fibrosis 2 receptor."				
R1	J. Biol. Chem. 275:10531-10536(2000).				

[illegible]

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GenVivo version 4.5
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3M protein - protein search, using sw model

Run on: August 12, 2002, 13:58:38 ; Search time 14.59 seconds

(without alignments)

820,037 E-Value cell updates/sec

Title: US-09-825-882-8
Perfect score: 309
Sequence: 1 MIFPLPILFSSLVVFFVIG.....FLSVFWMRWVWKEKRTSSP 309

Starting table:
Gapop 60.0 ; Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size: 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database: Swissprot_40.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	2.6	484	1	MURC_BUGAI
2	7	2.3	83	1	EXCA_BACSO
3	7	2.3	131	1	KV41_MOUSE
4	7	2.3	132	1	KV41_MOUSE
5	7	2.3	164	1	MUSB_CHLMU
6	7	2.3	284	1	APX_STRGR
7	7	2.3	286	1	FINO_ECOLI
8	7	2.3	320	1	PSST_PASMO
9	7	2.3	427	1	ESTC_RHLDI
10	7	2.3	437	1	ENIT_ECOLI
11	7	2.3	439	1	HNTE_ECOLI
12	7	2.3	492	1	CTP3_BROWA
13	7	2.3	552	1	NKRE_ECOLI
14	7	2.3	555	1	YI43_YEAST
15	7	2.3	568	1	NM02_MOUSE
16	7	2.3	568	1	NM02_MOUSE
17	7	2.3	574	1	WY16_YEAST
18	7	2.3	584	1	NIFA_RHLET
19	7	2.3	587	1	NM02_RAT
20	7	2.3	615	1	NITA_AZOGA
21	7	2.3	635	1	NKRE_HAEIN
22	7	2.3	686	1	KRC6_STADU
23	7	2.3	862	1	ADRE_GLOAB
24	7	2.3	896	1	PRSP_NEPSP
25	4	1.9	24	1	TRPA_HH11H
26	4	1.9	57	1	SICK1_MESMA
27	4	1.9	58	1	SICK2_MESMA
28	4	1.9	65	1	VY13_VACCC
29	4	1.9	76	1	ATP9_BAWMI
30	4	1.9	77	1	YGR0_BACPI
31	4	1.9	82	1	YGR0_BACPI
32	4	1.9	84	1	YGR0_BACPI
33	4	1.9	86	1	TXM1_MAJAT

34	6	1.9	87	1	NX14_HUMMU
35	6	1.9	87	1	NX16_HUMMU
36	6	1.9	87	1	YAL2_HA111
37	6	1.9	89	1	CYB_BKANA
38	6	1.9	102	1	U173_HHV
39	6	1.9	104	1	RL30_ELTIA
40	6	1.9	106	1	RST0_MOCBY
41	6	1.9	115	1	NM04_HUMMI
42	6	1.9	117	1	NM04_HUMMI
43	6	1.9	117	1	YCX2_CHIRE
44	6	1.9	120	1	GLH1_KAI
45	6	1.9	120	1	GLH2_KAI

ALIGNMENTS

RESULT 1
ID MURC_BUGAI STANJARD; PRT: 484 AA.
AC P57310;
DE 16-OCT-2001 (Rel. 40, last sequence update)
DE 16-OCT-2001 (Rel. 40, last annotation update)
DE UDP-N-acetylmutaric acid aldolase (EC 5.1.2.8) (UDP-N-acetylmutaric acid-L-alanine synthetase).
GN MURC OR M0215.
OS buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
syndiotic bacterium).
OC Fungi; Proteobacteria; Gamma subdivision; buchnera.
OX NCBI_TaxID:118099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN TOKYO 1998;
RX MEDLINE:20445173; PubMed:10936077;
FA Shigenobu S., Matsuda H., Hattori M., Sakaki Y., Ishikawa H.;
RI "Genome sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. APS.";
RL Nature 407:81-86(2000).
CC -!- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: ATP + UDP-N-acetylmutaric acid + L-alanine + ADP +
phosphate + UDP-N-acetylmutaric acid-L-alanine.
CC -!- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: BELONGS TO THE MURCOPF FAMILY.
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
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use by non-profit institutions as long as its content is in no way
modified and this statement is not removed, usurped by, and for commercial
purposes is allowed. See: http://www.ebi.ac.uk/seqdata/doc/seqdata.html
or send an email to: info@swissprot.ch).
CC EMBL: AP001118; BAW12941.1;
CC F330; F330; F330; F330; F330; F330; F330; F330; F330; F330;
CC pep1347; pep1347; pep1347; pep1347; pep1347; pep1347; pep1347; pep1347;
KW ATP-binding; Complete proteome.
FT NP_3100 125 131
FT SGNR000000 484 AA: 54-111 MW: 6635004.55059007 Da; pI: 5.44;
Query Match: 2.6% Score 87 DB 1; Length 484;
Post local similarity: 100.0% Prod. No. 4.27
Matches 8; Conserved 6; Mismatches 0; Indels 0; Gaps 0;
27 284 KRLKQIFL 291
DB 207 KRLKQIFL 214
RESULT 2
YXW1_BACSO


```

01 MAR-2002 (rel. 41, last sequence update)
01 MAR-2002 (rel. 41, last annotation update)
DE Phosphate transport system permease protein pstC.
GN pstC OR F0435.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellales.
OT Pasteurella.
OX NCBI_TaxID=247.
RN [1].
RF SEQUENCE FROM N.A.
RA MEDLINE:2145093; PubMed=11248100.
RA May H.J., Zhang Q., Li L.L., Paulian M.L., Whittam T.S., Kapur V.:
  "Complete genome sequence of Pasteurella multocida pm70."
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -1- FUNCTION: PART OF THE BINDING PROTEIN-DEPENDENT TRANSPORT SYSTEM
CC FOR PHOSPHATE. PRIMARY RESPONSIBLE FOR THE TRANSPORT OF THE
CC SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (by similarity).
CC -1- SIMILARITY: WITH INTERNAL MEMBRANE CARRIER OF OTHER BINDING
CC PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE CYSTIN
CC SUBFAMILY.
CC
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CC entities requires a license agreement (see http://www.ebi.ac.uk/ebd/
CC or send an email to license@ebi.ac.uk).
CC
DR EMBL: AB006079; AK02619.1;
DR InterPro: IPR000515; BPO.Transp.
DR Pfam: PF00528; BPO.Transp.1.
DR PROSITE: PS00402; BPO_TRANSP_INN_MEMBR_1.
KW Transport; Phosphate transport; Transmembrane; Inner membrane;
KW Complete proteome.
FT DOMAIN 1 27 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 28 50 POTENTIAL.
FT DOMAIN 51 80 PERIPLASMIC (POTENTIAL).
FT TRANSSEM 81 103 POTENTIAL.
FT DOMAIN 104 114 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 115 137 POTENTIAL.
FT DOMAIN 138 168 PERIPLASMIC (POTENTIAL).
FT TRANSSEM 169 191 POTENTIAL.
FT DOMAIN 192 229 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 230 252 POTENTIAL.
FT DOMAIN 253 287 PERIPLASMIC (POTENTIAL).
FT TRANSSEM 288 310 POTENTIAL.
FT DOMAIN 311 320 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 321 340 CYTOPLASMIC (POTENTIAL).
SEQUENCE 341 354 AA; 35405 MW; 198964D6277FE95A CRC64.

Query Match 2.48; Score 7; DR 1; Length 320;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID 15 VTEVIN 21
DB 248 VTEVIN 254
IIIIII
STANDARD; PRT; 427 AA.
01 MAR-2002 (rel. 41, created)
01 MAR-2002 (rel. 41, last sequence update)
01 MAR-2002 (rel. 41, last annotation update)
DE Phosphate transport system permease protein pstC.
GN pstC OR ML372.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellales.
OT Pasteurella.
OX NCBI_TaxID=247.
RN [1].
RF SEQUENCE FROM N.A.
RA MEDLINE:2145093; PubMed=11248100.
RA May H.J., Zhang Q., Li L.L., Paulian M.L., Whittam T.S., Kapur V.:
  "Complete genome sequence of Pasteurella multocida pm70."
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -1- FUNCTION: PART OF THE BINDING PROTEIN-DEPENDENT TRANSPORT SYSTEM
CC FOR PHOSPHATE. PRIMARY RESPONSIBLE FOR THE TRANSPORT OF THE
CC SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (by similarity).
CC -1- SIMILARITY: WITH INTERNAL MEMBRANE CARRIER OF OTHER BINDING
CC PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE CYSTIN
CC SUBFAMILY.
CC
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CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@ebi.ac.uk).
CC
DR EMBL: AB006079; AK02619.1;
DR InterPro: IPR000515; BPO.Transp.
DR Pfam: PF00528; BPO.Transp.1.
DR PROSITE: PS00402; BPO_TRANSP_INN_MEMBR_1.
KW Transport; Phosphate transport; Transmembrane; Inner membrane;
KW Complete proteome.
FT DOMAIN 1 27 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 28 50 POTENTIAL.
FT DOMAIN 51 80 PERIPLASMIC (POTENTIAL).
FT TRANSSEM 81 103 POTENTIAL.
FT DOMAIN 104 114 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 115 137 POTENTIAL.
FT DOMAIN 138 168 PERIPLASMIC (POTENTIAL).
FT TRANSSEM 169 191 POTENTIAL.
FT DOMAIN 192 229 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 230 252 POTENTIAL.
FT DOMAIN 253 287 PERIPLASMIC (POTENTIAL).
FT TRANSSEM 288 310 POTENTIAL.
FT DOMAIN 311 320 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 321 340 CYTOPLASMIC (POTENTIAL).
SEQUENCE 341 354 AA; 35405 MW; 198964D6277FE95A CRC64.

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01 MAR-2002 (rel. 41, last sequence update)
01 MAR-2002 (rel. 41, last annotation update)
DE Phosphate transport system permease protein pstC.
GN pstC OR ML372.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellales.
OT Pasteurella.
OX NCBI_TaxID=247.
RN [1].
RF SEQUENCE FROM N.A.
RA MEDLINE:2145093; PubMed=11248100.
RA May H.J., Zhang Q., Li L.L., Paulian M.L., Whittam T.S., Kapur V.:
  "Complete genome sequence of Pasteurella multocida pm70."
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -1- FUNCTION: PART OF THE BINDING PROTEIN-DEPENDENT TRANSPORT SYSTEM
CC FOR PHOSPHATE. PRIMARY RESPONSIBLE FOR THE TRANSPORT OF THE
CC SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (by similarity).
CC -1- SIMILARITY: WITH INTERNAL MEMBRANE CARRIER OF OTHER BINDING
CC PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE CYSTIN
CC SUBFAMILY.
CC
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CC
DR EMBL: AB006079; AK02619.1;
DR InterPro: IPR000515; BPO.Transp.
DR Pfam: PF00528; BPO.Transp.1.
DR PROSITE: PS00402; BPO_TRANSP_INN_MEMBR_1.
KW Transport; Phosphate transport; Transmembrane; Inner membrane;
KW Complete proteome.
FT DOMAIN 1 27 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 28 50 POTENTIAL.
FT DOMAIN 51 80 PERIPLASMIC (POTENTIAL).
FT TRANSSEM 81 103 POTENTIAL.
FT DOMAIN 104 114 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 115 137 POTENTIAL.
FT DOMAIN 138 168 PERIPLASMIC (POTENTIAL).
FT TRANSSEM 169 191 POTENTIAL.
FT DOMAIN 192 229 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 230 252 POTENTIAL.
FT DOMAIN 253 287 PERIPLASMIC (POTENTIAL).
FT TRANSSEM 288 310 POTENTIAL.
FT DOMAIN 311 320 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 321 340 CYTOPLASMIC (POTENTIAL).
SEQUENCE 341 354 AA; 35405 MW; 198964D6277FE95A CRC64.

Query Match 2.48; Score 7; DR 1; Length 327;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID 15 VTEVIN 21
DB 255 VTEVIN 261
IIIIII
STANDARD; PRT; 437 AA.
01 MAR-1995 (rel. 31, created)
01 NOV-1995 (rel. 32, last sequence update)
01 NOV-1995 (rel. 40, last annotation update)
DE High-affinity glutamate transporter (glutamate permease) (cat 1
DE system).
GN cat1 OR uc3a OR gdm OR h4415.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriales.
OT Escherichia.
OX NCBI_TaxID=562.
RN [1].
RF SEQUENCE FROM N.A.
RA MEDLINE:101655.
RA STRAIN K12 / MG1655.

```


NO.	SPERMATOPHYTES	400 Å.	400 Å.	WAVELENGTH	WAVELENGTH
F1	TRANSSEM	204	311	POTENTIAL	POTENTIAL
F1	TRANSSEM	327	417	POTENTIAL	POTENTIAL
F1	TRANSSEM	440	469	POTENTIAL	POTENTIAL
F1	TRANSSEM	471	481	POTENTIAL	POTENTIAL
F1	TRANSSEM	418	438	POTENTIAL	POTENTIAL
NO.	SPERMATOPHYTES	400 Å.	400 Å.	WAVELENGTH	WAVELENGTH

RN		171	VARIANTS CYP2E1*2 AND CYP2E1*3.
RP	MEDLINE:	9721162; PubMed:	9658190;
RX	In Vivo Oxidation M.; Johnson L.; Yue Y.Y.; Dahl M.L.; Tabone M.;		
KA	Alto S.; Albano E.; Ingelman-Sundberg M.		
RT	"Genetic polymorphism of human CYP2E1: characterization of two variant alleles."		
RI	Mol. Pharmacol.	51:370-376(1997).	
RN		[M]	
RP	VARIANT CYP2E1*4.		
KX	MEDLINE:	9911467; PubMed:	9918138;
KA	Fairbrother K.S.; Grove J.; de Wazters L.; Steimel D.L.; Hay C.P.;		
RA	Crespi G.L.; Daly A.K.		
RT	"Protection and characterization of novel polymorphisms in the CYP2E1 gene."		
RL	Pharmacogenetics	8:543-552(1998).	
CC	-1 FUNCTION: METABOLIZES SEVERAL PRECARNICINENS, PRODS., AND SOLVENTS TO REACTIVE METABOLITES.		
CC	-1+ CATALYTIC ACTIVITY: RH + reduced flavoprotein + O2 = ROH + oxidized flavoprotein + H(2)O.		
CC	-1+ SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.		
CC	-1+ INDUCTION: BY ETHANOL AND ISORHAZID.		
CC	-1+ SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.		
CC	! CATABOLISM: RAMP-Cytochrome p450 Allicle Nomenclature Committee; NON-CYP2E1 alleles?;		
CC	WWW: www.hsc.tamu.edu/cytcyto/p450.htm"		
CC			
CC	This Swiss Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL database.		
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CC			
EMBL:	J02625; AAA52743.1; -		
EMBL:	J02843; AAA52155.1; -		
EMBL:	A0192276; AA016001.1; -		
EMBL:	AF084225; AAD16754.1; -		
EMBL:	D60111; BA08796.1; -		
PIR:	A31949; A31949.		
PIR:	B25441; B25441.		
PIR:	A29660; A29660.		
HSSP:	P00179; IDT6.		
MIM:	124040; -		
InterPro:	IPR001128; Cyf_P450.		
PIfam:	PF00067; P450; 1.		
PRINTS:	PR00385; P450.		
PROSITE:	PS00086; CYTOCHROME_P450_1.		
FW	Classified as cytochrome b ₅ /cytochrome b ₅ Electron transport domain; Microsome; Endoplasmic reticulum; Polymorphism.		
FT	FTID VAR:	427	437
FT	VARIAAT	76	76
FT			
FT	VARIAAT	179	179
FT			
FT	VARIAAT	389	389
FT			
FT	CONFLICT	2	2
FT	CONFLICT	236	245
SC	SOURCE: 493 AA; 56849 MW; E00499E5A005664 OR 944		

001 Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
 002 Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus:
 003 Mus_taxid 10090;
 004 [1]
 005 SEQUENCE FROM N.A. (150908 N.R. IRE).
 006 MEDLINE: 9500920; PubMed: 7790986;
 007 Greenfield S., Collier M., Vidal S., Gros P.:
 008 "Identification and characterization of a second mouse Ntamp gene."
 009 Genomics 25:514-525(1995).
 010 [2]
 011 SEQUENCE FROM N.A. (150908 IRE).
 012 STRAIN IMA:
 013 Fleming M.D., Brown M.A., Su H.A., Garrick L.M., Garrick M.D.,
 014 Andrews N.C.:
 015 "Mouse natural resistance associated macrophage protein-2 (Ntamp2),
 016 a potential exon alternative splice variant."
 017 Submitted (Oct 1997) to the EMBL/Genbank/Trna databases.
 018 [3]
 019 VARIANT MK ARQ-185.
 020 MEDLINE: 97085245; PubMed: 9241278;
 021 Fleming M.D., Tienor C.C., III, Su M.A., Pomeroy D., Brier D.R.,
 022 Dietrich W.F., Andrews N.C.:
 023 "Macrocyclic anandamide mice have a mutation in Ntamp2, a candidate iron
 024 transporter gene."
 025 [4]
 026 FUNCTION: MACROPHAGE-SPECIFIC MEMBRANE TRANSPORT. IMPORTANT IN
 027 METAL TRANSPORT. IN PARTICULAR IRON.
 028 [5]
 029 SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 030 [6]
 031 ALTERNATIVE PRODUCTS: 2 ISOFORMS: ISOFORM IRE AND ISOFORM NON-
 032 IRE (SHOWN HERE) ARE PRODUCED BY ALTERNATIVE SPLICING.
 033 [7]
 034 TISSUE SPECIFICITY: EXPRESSED AT LOW LEVELS IN ALL TISSUES
 035 ANALYZED.
 036 [8]
 037 DISEASE DEFECTS IN SICKIA ARE THE CAUSE OF MICROCYTIC ANEMIA DUE
 038 (MS). HOMOTYGES MK/MK MICE HAVE HYPOCHROMIC MICROCYTIC ANEMIA DUE
 039 TO SEVERE DEFECTS IN INTESTINAL IRON ABSORPTION AND ERYTHROID IRON
 040 UTILIZATION.
 041 [9]
 042 SIMILARITY: BELONGS TO THE NtAMP FAMILY.
 043 [10]
 044 This SwissProt entry is copyright. It is produced through a collaboration
 045 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 046 the European Bioinformatics Institute. There are no restrictions on its
 047 use by non-profit institutions as long as its content is in no way
 048 modified and this statement is not removed, usage by and for commercial
 049 entities requires a license agreement (See: <http://www.ebi.ac.uk/infocentre/>
 050 or send an email to license@ebi.ac.uk).
 051 [11]
 052 EMBL: L3415; AAC12051.1;
 053 EMBL: AF039758; AAC14496.1;
 054 MGDB: MG11445279; Sct1142;
 055 InterPro: IP001046; Ntamp.
 056 Pfam: PF01566; Ntamp.1.
 057 PRINTS: PR00447; NtampSSCMP.
 058 Prodom: PD01861; Ntamp.1.
 059 Transport: Iron transport; Transmembrane; Glycoprotein;
 060 Alternative splicing; Disease mutation.
 061 Domain
 062 1 69
 063 cytoplasmic (POTENTIAL).
 064 Transmem
 065 70 90
 066 POTENTIAL.
 067 Extracellu
 068 91 95
 069 EXTRACELLULAR (POTENTIAL).
 070 Transmem
 071 96 117
 072 POTENTIAL.
 073 Extracellu
 074 118 154
 075 EXTRACELLULAR (POTENTIAL).
 076 Transmem
 077 155 175
 078 POTENTIAL.
 079 Extracellu
 080 176 179
 081 EXTRACELLULAR (POTENTIAL).
 082 Transmem
 083 180 194
 084 POTENTIAL.
 085 Extracellu
 086 195 208
 087 EXTRACELLULAR (POTENTIAL).
 088 Transmem
 089 209 229
 090 POTENTIAL.
 091 Extracellu
 092 230 255
 093 EXTRACELLULAR (POTENTIAL).
 094 Transmem
 095 256 276
 096 POTENTIAL.
 097 Extracellu
 098 277 301
 099 EXTRACELLULAR (POTENTIAL).
 100 Transmem
 101 302 322
 102 POTENTIAL.
 103 Extracellu
 104 323 360
 105 EXTRACELLULAR (POTENTIAL).
 106 Transmem
 107 361 381
 108 POTENTIAL.
 109 Extracellu
 110 382 408
 111 EXTRACELLULAR (POTENTIAL).
 112 Transmem
 113 409 429
 114 POTENTIAL.

FT DOMAIN 430 440 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 441 461 POTENTIAL.
 FT DOMAIN 462 482 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 483 503 POTENTIAL.
 FT DOMAIN 504 506 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 507 527 POTENTIAL.
 FT DOMAIN 528 568 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 569 589 N-LINKED (GLYNA...) (POTENTIAL).
 FT CARBOHYD 590 599 N-LINKED (GLYNA...) (POTENTIAL).
 FT CARBOHYD 600 609 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 610 619 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 620 629 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 630 639 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 640 649 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 650 659 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 660 669 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 670 679 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 680 689 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 690 699 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 700 709 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 710 719 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 720 729 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 730 739 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 740 749 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 750 759 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 760 769 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 770 779 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 780 789 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 790 799 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 800 809 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 810 819 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 820 829 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 830 839 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 840 849 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 850 859 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 860 869 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 870 879 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 880 889 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 890 899 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 900 909 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 910 919 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 920 929 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 930 939 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 940 949 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 950 959 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 960 969 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 970 979 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 980 989 N-LINKED (GLYNA...) (POTENTIAL).
 FT TRANSMEM 990 999 N-LINKED (GLYNA...) (POTENTIAL).

Query Match
 Best Local 7; Conservative 100.0%; Score 71.08; Length 568;
 Matches 7; Mismatches 0; Indels 0; Gaps 0;
 QY 58 L1WILL 64
 1111111
 DB 104 L1WILL 110
 Search completed: August 12, 2002, 14:02:05
 Job time: 207 sec

Query Match 2.000 Score 72.000 Length 207
 Best Local Similarity 100.000 Prod. No. 4.63
 Matches 72 Conservative 02 Mismatches 02 Indels 02 Gaps 02

QY 58 ILWILLE 64
 DB 7 ILWILLE 13

RESULT 2

US-09-095-649-16
 Sequence 16, Application US/09095649
 Patent No. 6,242,213
 GENERAL INFORMATION:
 APPLICANT: Anderson, Dirk M.
 APPLICANT: Marosowsky, Eugene
 TITLE OF INVENTION: Ligand for Receptor Activation of NF-kappaB
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation, Law Department
 STREET: 11 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZITE: 09101
 COMPUTER RELEVABLE FORM:
 MEDIUM TYPE: floppy disk
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: USN 09/095-649
 FILING DATE: 14 OCTOBER 1997
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USN 09/091-16
 FILING DATE: 07 MARCH 1997
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USN 08/772-840
 FILING DATE: 23 DECEMBER 1996
 CLASSIFICATION:
 ALTERNATIVE/AGENT INFORMATION:
 NAME: Lockhart, Patricia Anne
 REGISTRATION NUMBER: 34,693
 REFERENCE/DOCKET NUMBER: 2801-A
 TELEPHONE: (206)587-0430
 TELEFAX: (206)243-0644
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 MOLECULE TYPE: protein
 US-09-095-649-16

Query Match 2.000 Score 72.000 Length 207
 Best Local Similarity 100.000 Prod. No. 4.63
 Matches 72 Conservative 02 Mismatches 02 Indels 02 Gaps 02

QY 58 ILWILLE 64
 DB 7 ILWILLE 13

Query Match 3
 US-09-215-649A-16
 Sequence 16, Application US/09215649A
 Patent No. 6,271,449
 GENERAL INFORMATION:
 APPLICANT: Anderson, Dirk M.
 APPLICANT: Marosowsky, Eugene
 TITLE OF INVENTION: Receptor Activation of NF-kappaB
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation, Law Department
 STREET: 11 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZITE: 09101
 COMPUTER RELEVABLE FORM:
 MEDIUM TYPE: floppy disk
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/215-649A
 FILING DATE: 17 JUNE 1998
 CLASSIFICATION: unknown
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/095-649
 FILING DATE: unknown
 APPLICATION NUMBER: USN 08/814-509
 FILING DATE: 07 MARCH 1997
 APPLICATION NUMBER: USN 08/772-840
 FILING DATE: 23 DECEMBER 1996
 NAME: Lockhart, Patricia Anne
 REGISTRATION NUMBER: 34,693
 REFERENCE/DOCKET NUMBER: 2801-A
 TELEPHONE: (206)587-0430
 TELEFAX: (206)243-0644
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 16:
 US-09-215-649A-16

Query Match 2.000 Score 72.000 Length 207
 Best Local Similarity 100.000 Prod. No. 4.63
 Matches 72 Conservative 02 Mismatches 02 Indels 02 Gaps 02

QY 58 ILWILLE 64
 DB 7 ILWILLE 13

RESULT 4
 US-09-320-424-25
 Sequence 25, Application US/09320424
 Patent No. 6,284,256
 GENERAL INFORMATION:
 APPLICANT: Willey, Steven K.
 APPLICANT: Goodman, Raymond G.
 TITLE OF INVENTION: Cytokine that Induces Apoptosis
 FILE REFERENCE: 2845 E
 CURRENT FILING DATE: 09/09/320-424
 EARLIER FILING DATE: 1999-05-26
 EARLIER APPLICATION NUMBER: 09/190-046
 EARLIER FILING DATE: 1998-11-10
 EARLIER APPLICATION NUMBER: 09/048-041

Query Match 2.000 Score 72.000 Length 207
 Best Local Similarity 100.000 Prod. No. 4.63
 Matches 72 Conservative 02 Mismatches 02 Indels 02 Gaps 02

QY 58 ILWILLE 64
 DB 7 ILWILLE 13

? EARLIER FILING DATE: 1998-03-26
 ? EARLIER APPLICATION NUMBER: 08/670,454
 ? EARLIER FILING DATE: 1996-06-25
 ? EARLIER APPLICATION NUMBER: 08/548,468
 ? EARLIER FILING DATE: 1995-11-01
 ? EARLIER APPLICATION NUMBER: 08/496,632
 ? EARLIER FILING DATE: 1995-06-29
 ? NUMBER OF SEQ. ID NOS: 25
 ? SOFTWARE: Patent In Ver. 2.0
 ? SEQ. ID NO: 25
 ? LENGTH: 20
 ? TYPE: PRT
 ? ORGANISM: Homo sapiens
 US-09-820-424-25

Query Match 2.88: Score 7: DB 4: Length 20:
 Best Local Similarity 100.0%: Prod. No. 4.6:
 Matches 7: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 58 ILWILL 64
 DB 7 ILWILL 13

RESULT 5
 US-08-518-845-5
 ? Sequence 5: Application US/08/51845
 ? Patent No. 6017754
 ? GENERAL INFORMATION:
 ? APPLICANT: CHESTNUT, JONATHAN D.
 ? APPLICANT: HEEFER, JAMES P.
 ? TITLE OF INVENTION: ROBOT SYSTEM FOR LOCATING AND
 ? TITLE OF INVENTION: IDENTIFYING POKERFISH CELLS TRANSFECTED WITH GENES AND
 ? TITLE OF INVENTION: VECTORS, HOST CELLS AND METHODS THEREOF
 ? NUMBER OF SEQUENCES: 6
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: SQUITY, SCOTT, MURPHY & PRESSER
 ? STREET: 400 GARDEN CITY PLAZA
 ? CITY: GARDEN CITY
 ? STATE: NEW YORK
 ? COUNTRY: USA
 ? ZIP: 11530
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: FLOPPY disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Patent In Release #1.0, Version #1.39
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/518,835
 ? FILING DATE: 24-NOV-1995
 ? CLASSIFICATION: 435
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: DIGILLO, FRANK S.
 ? REGISTRATION NUMBER: 31,446
 ? REFERENCE/EXCERPT NUMBER: 11094
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (516) 742-4443
 ? TELEFAX: (516) 742-4366
 ? INFORMATION FOR SEQ. ID NOS: 5:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 21 amino acids
 ? TYPE: amino acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 US-08-518-845-5

Query Match 2.88: Score 7: DB 3: Length 21:
 Best Local Similarity 100.0%: Prod. No. 4.8:
 Matches 7: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 58 ILWILL 64

DB 7 ILWILL 13

RESULT 6
 US-07-644-278-21
 ? Sequence 21: Application US/07/644278
 ? Patent No. 5580101
 ? GENERAL INFORMATION:
 ? APPLICANT: COHEN, CARY L.
 ? APPLICANT: CO, Man Sung
 ? APPLICANT: SCHNEIDER, William P.
 ? APPLICANT: LAMOLLET, Nicholas P.
 ? APPLICANT: CORLINC, Kathleen L.
 ? APPLICANT: SELICK, Harold E.
 ? TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 ? NUMBER OF SEQUENCES: 11
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Townsend and Townsend Kiorito and Crow
 ? STREET: 379 Lytton Avenue
 ? CITY: Palo Alto
 ? STATE: California
 ? COUNTRY: US
 ? ZIP: 94301
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: FLOPPY disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Patent In Release #1.0, Version #1.25
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/07/644,278
 ? FILING DATE: 19 DEC-1990
 ? CLASSIFICATION: 424
 ? ERROR APPLICATION DATA:
 ? APPLICATION NUMBER: US 07/590,274
 ? FILING DATE: 28 SEP-1990
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US 07/310,252
 ? FILING DATE: 13-FEB-1989
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US 07/290,975
 ? FILING DATE: 28-DEC-1988
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Smith, William M.
 ? REGISTRATION NUMBER: 30,223
 ? REFERENCE/EXCERPT NUMBER: 11822-002600
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (415) 326-2420
 ? INFORMATION FOR SEQ. ID NOS: 21:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 126 amino acids
 ? TYPE: amino acid
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: protein
 US 07 644 278 21

Query Match 2.88: Score 7: DB 1: Length 126:
 Best Local Similarity 100.0%: Prod. No. 24:
 Matches 7: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 58 ILWILL 64
 DB 7 ILWILL 13

RESULT 7
 US-08-477-728-21
 ? Sequence 21: Application US/08/477728
 ? Patent No. 5585089
 ? GENERAL INFORMATION:
 ? APPLICANT: QUINN, Cary L.

```

1 APPLICANT: SCHNEIDER, William F.
2 APPLICANT: SELLER, Harold E.
3 TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
4 NUMBER OF SEQUENCES: 114
5 CORRESPONDENCE ADDRESS:
6 ADDRESSEE: Townsend and Townsend and Crew LLP
7 STREET: Two International Center, 8th Floor
8 CITY: Palo Alto
9 STATE: California
10 COUNTRY: US
11 ZIP: 94301
12 COMPUTER RELEASABLE FORM:
13 MEDIUM TYPE: Floppy disk
14 OPERATING SYSTEM: pc dos/MS-DOS
15 SOFTWARE: Patent Release #1.0, Version #1.25
16 PUBLICATION DATE: 07/09/1995
17 PUBLICATION NUMBER: US 07/590,274
18 APPLICATION DATE: 07/09/1995
19 APPLICATION NUMBER: US 07/410,292
20 PRIORITY DATE: 19 DEC 1990
21 PRIORITY NUMBER: US 07/290,975
22 PRIORITY APPLICATION DATA:
23 FILING DATE: 28 SEP 1990
24 FILING NUMBER: US 07/290,975
25 NAME: Smith, William M
26 REGISTRATION NUMBER: 40,224
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: (415) 426-2400
29 TELEFAX: (415) 426-2422
30 INFORMATION FOR SEQ ID NO: 21:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 126 amino acids
33 TYPE: amino acid
34 TOPOLOGY: linear
35 MOLECULE TYPE: protein
36 US-09-825-882-8
37
38 Query Match: 2.98, Score 71, DB 1, Length 126;
39 Host Local Similarity: 100.0%; Prod. No. 24;
40 Matches: 7; Conservation: 0; Mismatches: 0; Indels: 0; Gaps: 0;
41
42 QY 58 ILWILL 64
43 DB 7 ILWILL 14
44
45 RESULT 9
46 US-09-825-882-8
47 Sequence 21, Application US/09/474/040
48 Patent No. 565,472
49 GENERAL INFORMATION:
50 APPLICANT: GIBSON, Gary L.
51 APPLICANT: N. Man, Sonu
52 APPLICANT: SCHNEIDER, William F.
53 APPLICANT: LANESE, Nicholas P.
54 APPLICANT: GELINCH, Kathleen E.
55 APPLICANT: SELLER, Harold E.
56 TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
57 NUMBER OF SEQUENCES: 114
58 CORRESPONDENCE ADDRESS:
59 ADDRESSEE: Townsend and Townsend and Crew
60 STREET: 879 Lydon Avenue
61 CITY: Palo Alto
62 STATE: California
63 COUNTRY: US
64 ZIP: 94301
65 COMPUTER RELEASABLE FORM:
66 MEDIUM TYPE: Floppy disk
67 OPERATING SYSTEM: pc dos/MS-DOS
68
69 US-09-825-882-8

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1 CITY: Palo Alto
2 STATE: California
3 COUNTRY: US
4 ZIP: 94301
5 COMPUTER RELEASABLE FORM:
6 MEDIUM TYPE: Floppy disk
7 OPERATING SYSTEM: pc dos/MS-DOS
8 SOFTWARE: Patent Release #1.0, Version #1.25
9 CURRENT APPLICATION DATA:
10 APPLICATION NUMBER: US/09/474,040
11 FILING DATE: 07-JUN-1995
12 CLASSIFICATION: 546
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: US 07/434,278
15 FILING DATE: 19 DEC 1990
16 APPLICATION NUMBER: US 07/590,274
17 PRIORITY DATE: 28-SEP-1990
18 PRIORITY APPLICATION DATA:
19 APPLICATION NUMBER: US 07/410,292
20 FILING DATE: 13 FEB 1999
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: US 07/290,975
23 FILING DATE: 28 DEC 1998
24 ADDRESS/Agent INFORMATION:
25 NAME: Smith, William M
26 REGISTRATION NUMBER: 40,224
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: (415) 426-2400
29 TELEFAX: (415) 426-2422
30 INFORMATION FOR SEQ ID NO: 21:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 126 amino acids
33 TYPE: amino acid
34 TOPOLOGY: linear
35 MOLECULE TYPE: protein
36 US-09-825-882-8
37
38 Query Match: 2.98, Score 71, DB 1, Length 126;
39 Host Local Similarity: 100.0%; Prod. No. 24;
40 Matches: 7; Conservation: 0; Mismatches: 0; Indels: 0; Gaps: 0;
41
42 QY 58 ILWILL 64
43 DB 7 ILWILL 14
44
45 RESULT 9
46 US-09-825-882-8
47 Sequence 21, Application US/09/474/040
48 Patent No. 565,472
49 GENERAL INFORMATION:
50 APPLICANT: GIBSON, Gary L.
51 APPLICANT: N. Man, Sonu
52 APPLICANT: SCHNEIDER, William F.
53 APPLICANT: LANESE, Nicholas P.
54 APPLICANT: GELINCH, Kathleen E.
55 APPLICANT: SELLER, Harold E.
56 TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
57 NUMBER OF SEQUENCES: 114
58 CORRESPONDENCE ADDRESS:
59 ADDRESSEE: Townsend and Townsend and Crew
60 STREET: 879 Lydon Avenue
61 CITY: Palo Alto
62 STATE: California
63 COUNTRY: US
64 ZIP: 94301
65 COMPUTER RELEASABLE FORM:
66 MEDIUM TYPE: Floppy disk
67 OPERATING SYSTEM: pc dos/MS-DOS
68
69 US-09-825-882-8

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8  SETWARE: Patent in Release #1.0, Version #1.25
9  CURRENT APPLICATION DATA:
10  APPLICATION NUMBER: US/08/484,209
11  FILING DATE: 7-JUN-1995
12  CLASSIFICATION: 4.24
13  PRIOR APPLICATION DATA:
14  APPLICATION NUMBER: US 07/614,278
15  FILING DATE: 19-DEC-1990
16  PRIOR APPLICATION DATA:
17  APPLICATION NUMBER: US 07/590,274
18  FILING DATE: 28-SEP-1990
19  PRIOR APPLICATION DATA:
20  APPLICATION NUMBER: US 07/710,252
21  FILING DATE: 13-FEB-1989
22  PRIOR APPLICATION DATA:
23  APPLICATION NUMBER: US 07/290,975
24  FILING DATE: 28-DEC-1988
25  ATTORNEY/AGENT INFORMATION:
26  NAME: Smith, William M
27  REGISTRATION NUMBER: 30,224
28  REFERENCE/SEQUENCE NUMBER: 11824-002610
29  TELECOMMUNICATION INFORMATION:
30  TELEPHONE: (415) 426-2400
31  TELEFAX: (415) 426-2422
32  INFORMATION FOR SEQ ID NO: 21:
33  SEQUENCE CHARACTERISTICS:
34  LENGTH: 126 amino acids
35  TYPE: amino acid
36  TOPOLOGY: linear
37  MOLECULE TYPE: protein
38  US 08/484,209 21

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Query Match: 2.48; Score 7; DB 1; Length 126;
 Best Local Similarity: 100.0%; Prod. No. 24;
 Matches: 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 58 ILWILL 64
10 7 ILWILL 13

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8  RESULT 10
9  US-08-656-586 6
10  Sequence 6; Application 05/0845786
11  Patent No. 684457
12  GENERAL INFORMATION:
13  APPLICANT: Tso, J. Yun
14  APPLICANT: Goto, Michael S.
15  APPLICANT: Andsotti, Claudio
16  TITLE OF INVENTION: Mutated No. 5844597activation IgG2 domains and
17  TITLE OF INVENTION: Act 1 G2A Antibodies Incorporating 1 G2A
18  NUMBER OF SEQUENCES: 13
19  CORRESPONDENCE ADDRESS:
20  ADDRESSEE: Townsend and Townsend and Crew LLP
21  STREET: Two Embarcadero Center, Eighth Floor
22  CITY: San Francisco
23  STATE: California
24  COUNTRY: USA
25  ZIP: 94111-6444
26  COMPUTER READABLE FORM:
27  MEDIUM TYPE: Floppy disk
28  COMPUTER: IBM pc compatible
29  OPERATING SYSTEM: PC DOS/MS-DOS
30  SOFTWARE: Patent in Release #1.0, Version #1.00
31  CURRENT APPLICATION DATA:
32  APPLICATION NUMBER: US/08/484,596
33  FILING DATE: 31-MAY-1996
34  CLASSIFICATION: 5.80
35  ATTORNEY/AGENT INFORMATION:
36  NAME: Jacobsen, Joseph O.
37  REGISTRATION NUMBER: 47,505
38  REFERENCE/SEQUENCE NUMBER: 11824-002100S

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8  TELECOMMUNICATION INFORMATION:
9  TELEPHONE: (415) 576-0200
10  TELEFAX: (415) 576-0400
11  INFORMATION FOR SEQ ID NO: 6:
12  SEQUENCE CHARACTERISTICS:
13  LENGTH: 126 amino acids
14  TYPE: amino acid
15  TOPOLOGY: linear
16  MOLECULE TYPE: protein
17  US 08 656 586 6

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Query Match: 2.48; Score 7; DB 1; Length 126;
 Best Local Similarity: 100.0%; Prod. No. 24;
 Matches: 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 58 ILWILL 64
10 7 ILWILL 13

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8  RESULT 11
9  US-08-484-597-21
10  Sequence 21; Application 05/0844547
11  Patent No. 6180470
12  GENERAL INFORMATION:
13  APPLICANT: QUREN, Gary L.
14  APPLICANT: CO, Max Sheng
15  APPLICANT: STIMBBER, William P.
16  APPLICANT: LANDOLFI, Nicholas P.
17  APPLICANT: CULLIRICH, Kathleen L.
18  APPLICANT: SELICK, Harold E.
19  TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
20  NUMBER OF SEQUENCES: 113
21  CORRESPONDENCE ADDRESS:
22  ADDRESSEE: Townsend and Townsend Kiewit and Crew
23  STREET: 379 Lytton Avenue
24  CITY: Palo Alto
25  STATE: California
26  COUNTRY: US
27  ZIP: 94301
28  COMPUTER READABLE FORM:
29  MEDIUM TYPE: Floppy disk
30  COMPUTER: IBM pc compatible
31  OPERATING SYSTEM: PC DOS/MS-DOS
32  SOFTWARE: Patent in Release #1.0, Version #1.25
33  CURRENT APPLICATION DATA:
34  APPLICATION NUMBER: US/08/484,537
35  FILING DATE:
36  CLASSIFICATION:
37  PRIOR APPLICATION DATA:
38  APPLICATION NUMBER: US 07/319,252
39  FILING DATE: 19-DEC-1990
40  PRIOR APPLICATION DATA:
41  APPLICATION NUMBER: US 07/590,274
42  FILING DATE: 28-SEP-1990
43  PRIOR APPLICATION DATA:
44  APPLICATION NUMBER: US 07/710,252
45  FILING DATE: 13-FEB-1989
46  PRIOR APPLICATION DATA:
47  APPLICATION NUMBER: US 07/290,975
48  FILING DATE: 28-DEC-1988
49  ATTORNEY/AGENT INFORMATION:
50  NAME: Smith, William M
51  REGISTRATION NUMBER: 30,224
52  REFERENCE/SEQUENCE NUMBER: 11824-002600
53  TELECOMMUNICATION INFORMATION:
54  TELEPHONE: (415) 426-2400
55  TELEFAX: (415) 426-2422
56  INFORMATION FOR SEQ ID NO: 21:
57  SEQUENCE CHARACTERISTICS:
58  LENGTH: 126 amino acids
59  TYPE: amino acid
60  TOPOLOGY: linear

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1 MILESTONE TYPE: F-0000

US-09-825-882-8

2009 Mar 07 2:00 Score 72 DB 4 Length 1282
 Host Local Similarity 100.00 Prod. No. 24
 Matches 72 Conservation 0 Mismatches 0 Indels 0 Gaps 0

27 58 L1WILL 64

28 7 L1WILL 13

RESULT 14

US-09-825-882-8

1 Applicant: Knapik, John

2 Title of Invention: VARIATION OF IMMUNOLOGICAL

3 NUMBER OF SEQUENCES: 108

4 ADDRESS: 225 Franklin Street, Suite 4100

5 CITY: Boston

6 STATE: MA

7 COUNTRY: USA

8 ZIP: 02110-2804

9 COMPUTER READABLE FORM:

10 MEDIUM TYPE: floppy disk

11 SOFTWARE: Patent in Release #1.0, Version #1.008

12 CURRENT APPLICATION DATA:

13 APPLICANT: VASQUEZ, MAXIMILIANO

14 FILING DATE: 01 Dec 1994

15 ATTORNEY/AGENT INFORMATION:

16 NAME: Clark, Paul T.

17 REGISTRATION NUMBER: 40,162

18 FEE: \$2,000.00

19 TELECOMMUNICATION INFORMATION:

20 TELEPHONE: (617) 542-5070

21 TELEFAX: (617) 542-5070

22 TELETYPE: 200154

23 INFORMATION FOR SEQ ID NO: 6:

24 SEQUENCE CHARACTERISTICS:

25 LENGTH: 128 amino acids

26 TYPE: amino acid

27 STRANDEDNESS: not relevant

28 TOPOLOGY: linear

29 MOLECULE TYPE: protein

US-09-825-882-8

US-09-825-882-8

US-09-825-882-8

1 APPLICANT: Knapik, John

2 Title of Invention: VARIATION OF IMMUNOLOGICAL

3 NUMBER OF SEQUENCES: 108

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9 COMPUTER READABLE FORM:

10 MEDIUM TYPE: floppy disk

11 SOFTWARE: Patent in Release #1.0, Version #1.008

12 CURRENT APPLICATION DATA:

13 APPLICANT: VASQUEZ, MAXIMILIANO

14 FILING DATE: 01 Dec 1994

15 ATTORNEY/AGENT INFORMATION:

16 NAME: Clark, Paul T.

17 REGISTRATION NUMBER: 40,162

18 FEE: \$2,000.00

19 TELECOMMUNICATION INFORMATION:

20 TELEPHONE: (617) 542-5070

21 TELEFAX: (617) 542-5070

22 TELETYPE: 200154

23 INFORMATION FOR SEQ ID NO: 6:

24 SEQUENCE CHARACTERISTICS:

25 LENGTH: 128 amino acids

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28 TOPOLOGY: linear

29 MOLECULE TYPE: protein

US-09-825-882-8

US-09-825-882-8

US-09-825-882-8

US-09-825-882-8

US-09-825-882-8

US-09-825-882-8

US-09-825-882-8

US-09-825-882-8

US-09-825-882-8

US-09-825-882-8

US-09-825-882-8

US-09-825-882-8

Query Match 2.38; Score 7; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 L1WVILL.64
|||||
DB 7 L1WVILL.13

RESULT 15
PCT-US95-15716-6
Sequence 6, Application PC/TUS9515716
GENERAL INFORMATION:
APPLICANT: Berdoz, Jose
TITLE OF INVENTION: PCR AMPLIFICATION OF PEAPRANGED GENOMIC
TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Richardson
STREET: 225 Franklin Street, Suite 3100
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15716
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/348,548
FILING DATE: 01-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06132/000001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-5070
TELEX: 200154
INFORMATION FOR SEQ. ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT US95-15716-6

Query Match 2.38; Score 7; DB 5; Length 128;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 L1WVILL.64
|||||
DB 7 L1WVILL.13

Search completed: August 12, 2002, 14:00:02
Job time: 249 sec

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[illegible]

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 Db 545 TATTCTGTCAAGATACAAATTTCTGACGCATATTTCTGTAAAANCAACAI 486

485 TAA...TATAGTTTGGCTTCTGTAAGAGAGTCTTAACTATATGTAAGAGTATTTCTTT 479

428 CTTAGTACTCTGAATGCTTTAAAGCA1AAAAAAATCTGTATATAAATTTATTTTGGTA 469

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[illegible]

735 **gatgatacatttggatttttgaagctctggaaacaaacctctctctatctctctaa** 794

[illegible]

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PSM 12
BH280188/c

[illegible]

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90-98	Norway	Fat	Eukaryotic
90-99	Norway	Fat	Eukaryotic
90-100	Norway	Fat	Eukaryotic

REFERENCE	AUTHORS
1 (bases 1 to 610)	Katus.
	Shatsman, S., 1964, 1965, 1966, 1967, 1968, 1969, 1970, 1971, 1972, 1973, 1974, 1975, 1976, 1977, 1978, 1979, 1980, 1981, 1982, 1983, 1984, 1985, 1986, 1987, 1988, 1989, 1990, 1991, 1992, 1993, 1994, 1995, 1996, 1997, 1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 263

Journal and Editor's M.	Title	Journal	Comment
Kat. Rev. and Sequences from Literary Choral and Prose Segment	Published (1999)	Other	Other

Department of Biotechnology
The Institute for Genetic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
and Tel: 301-980-0000

Fax: 401 838 0208
Email: s.chao@iitd.ac.in
Clones are derived from the rat BAC library CHOK1.240

KE (trans:0.5,4.0,KE), 15/15, reference contig. Inserted by Ref. This library was constructed for full-length clones and was constructed by cDNA with subclones (Baito Alto, A). Note: This is a NIH Map Library.

NAME / CNT

117 1 126 9 229 1

Query Match

Score 496 DB 10 Length 677

Best Local Similarity

100.0% Prod. No. 2,9616

Mismatch

0 Mismatch 0 Indels 0 Gaps 0

27

117 1 126 9 229 1

DEFINITION

AM260406 400 bp mRNA linear EST 40-DIC-1999

Accession

AM260406

Version

1

KEYWORDS

EST

ORGANISM

human

REFERENCE

1 (bases 1 to 400)

AUTHORS

Zhou, J. K., Yan, X. L., Han, F. C., Gu, D. X., Hou, Y., Yan, Q. J., and Su

COMMENT

Insertion and deletion differentially expressed in mRNA sequence

FEATURES

Location/Qualifiers

ORIGIN

117 1 126 9 229 1

BASE COUNT

109 a 126 c 108 g 64 t

ORIGIN

117 1 126 9 229 1

BASE COUNT

109 a 126 c 108 g 64 t

ORIGIN

117 1 126 9 229 1

BASE COUNT

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ORIGIN

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BASE COUNT

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ORIGIN

117 1 126 9 229 1

BASE COUNT

109 a 126 c 108 g 64 t

ORIGIN

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BASE COUNT

109 a 126 c 108 g 64 t

ORIGIN

117 1 126 9 229 1

BASE COUNT

109 a 126 c 108 g 64 t

ORIGIN

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BASE COUNT

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ORIGIN

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BASE COUNT

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ORIGIN

117 1 126 9 229 1

BASE COUNT

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ORIGIN

117 1 126 9 229 1

BASE COUNT

109 a 126 c 108 g 64 t

ORIGIN

117 1 126 9 229 1

ORGANISM

Human sapiens

REFERENCE

1 (bases 1 to 443)

AUTHORS

Dias, M. T., de, Faria, C. V., de, W. J., de, Almeida, S., de, Jones, M. R.,

NAME / CNT

117 1 126 9 229 1

Query Match

Score 411 DB 10 Length 343

Best Local Similarity

100.0% Prod. No. 2,9616

Mismatch

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117 1 126 9 229 1

DEFINITION

AM260406 400 bp mRNA linear EST 40-DIC-1999

Accession

AM260406

Version

1

KEYWORDS

EST

ORGANISM

human

REFERENCE

1 (bases 1 to 400)

AUTHORS

Zhou, J. K., Yan, X. L., Han, F. C., Gu, D. X., Hou, Y., Yan, Q. J., and Su

COMMENT

Insertion and deletion differentially expressed in mRNA sequence

FEATURES

Location/Qualifiers

ORIGIN

117 1 126 9 229 1

BASE COUNT

109 a 126 c 108 g 64 t

ORIGIN

117 1 126 9 229 1

BASE COUNT

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BASE COUNT

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ORIGIN

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BASE COUNT

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BASE COUNT

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BASE COUNT

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BASE COUNT

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ORIGIN

117 1 126 9 229 1

BASE COUNT

109 a 126 c 108 g 64 t

ORIGIN

117 1 126 9 229 1

BASE COUNT

109 a 126 c 108 g 64 t

ORIGIN

117 1 126 9 229 1

(http://www.ncbi.nlm.nih.gov/ncbi/pools/seq/seq1.412.asp) 219
 seq1.412:2000-03-24:14 1)

Seq primer: puc18 forward
 High quality sequence start: 41
 High quality sequence stop: 468
 Location/Qualifiers

FEATURES

1..409
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 /db_xref "taxon:9606"
 /clone_lib "H00127"
 /env_state "Adult"

/note "Cloned: breast normal; Vector: puc18; Site 1: Small; Site 2: Small; A mini-library was made by cloning products derived from ORFESTS PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 150 a 61 c 72 g 126 t
 ORIGIN

Query Match 2.2% Score 20; DB 9; Length 409;
 Best Local Similarity 100.0%; Prod. No. 73;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 346 TATTTCCTCCTAATAA 367
 DB 113 TATTTCCTCCTAATAA 94

RESULT 14
 ORG: HUMAN
 LOCUS: tetraodon nitroviridis genome survey sequence post-3' end of clone
 DEFINITION: cDNA of library 6 from Tetraodon nitroviridis, genomic survey
 sequence.

ACCESSION AT264560.1 GI:7986261
 VERSION 1
 KEYWORDS GSS: genomic survey sequence;
 SOURCE Tetraodon nitroviridis
 ORGANISM Tetraodon nitroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 Tetraodontidae; Tetraodon.
 1 (bases 1 to 489)

Authors: Roussell, L., Billault, A., Queller, F., South, W., Bernot, A. and
 Weissbach, J.

Characterization and repeat analysis of the compact genome of the
 freshwater putative fish Tetraodon nitroviridis
 Unpublished
 2 (bases 1 to 489)

Authors: Roussell, L., Billault, A., Queller, F., Bernot, A., Fisher, C.,
 South, W. and Weissbach, J.

Human gene number estimate provided by genome wide analysis using
 Tetraodon nitroviridis DNA sequence
 Unpublished
 3 (bases 1 to 489)

Journal Reference

Authors: Roussell, L., Billault, A., Queller, F., Bernot, A., Fisher, C.,
 South, W. and Weissbach, J.

Direct submission
 submitted (17-AUG-2000) to the EMBL/GenBank/CCDS databases
 This sequence is a single read and was generated as part of a large
 scale clone-end sequencing project of the Tetraodon nitroviridis
 genome. For more information, please take a look at
 http://www.ncbi.nlm.nih.gov/ncbi/pools/seq/seq1.412.asp

FEATURES

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 /db_xref "taxon:99883"
 /clone "H05014"

/clone_lib "G"
 /note "Genoscope sequence ID: G083064707SP1 end:
 puc ori"

BASE COUNT 166 a 101 c 64 g 150 t
 ORIGIN

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 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 TTAATAATTAAGAGTAAGA 243
 DB 329 TTAATACTTAAAGAGTAAGA 310

RESULT 15
 ORG: HUMAN
 LOCUS: 504 bp DNA linear GSS: 20 JUN 1998
 DEFINITION: C1T-HSP-389512.T1R C1T-HSP Homo sapiens genomic clone 389512, DNA
 sequence.

ACCESSION H54977
 VERSION 1
 KEYWORDS GSS:
 SOURCE human
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
 1 (bases 1 to 504)

Authors: Adams, M.D., Kounstley, S.D., Field, C.E., Bass, S., Linbo, K., Golden,
 J.K., Berry, K., Granger, D., Sub, E., Wible, C., Shizuya, H., Simon, M.
 and Venter, A.J.

Use of a random BAC End Sequence database for Sequence Ready Map
 building
 Unpublished (1997)

Comments: C1T-HSP-389512.T1R
 Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208

Email: madas@tigr.org
 Clones are available from Research Genetics (Info: resgen.com), BAC
 end search page:
 http://www.tigr.org/ftp/ftp3.1.1/Genomes/Chimp/seq/seq1.412.asp
 Seq primer: M13 Reverse
 Class: BAC ends.
 Location/Qualifiers

1..504
 /organism "Homo sapiens"
 /db_xref "taxon:9606"
 /clone_lib "H00127"
 /env_state "Adult"

/note "Cloned: breast normal; Vector: puc18; Site 1: Small; Site 2:
 Small; A mini-library was made by cloning products derived from ORFESTS PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 186 a 88 c 71 g 159 t
 ORIGIN

Query Match 2.2% Score 20; DB 12; Length 504;
 Best Local Similarity 100.0%; Prod. No. 75;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 513 GATTTTATTTTAAATATAT 522
 DB 420 AATCTACTTTTCAAAATATCA 401

Search completed: August 12, 2002, 14:11:58
1 to 4 lines, 5000 lines
